

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 ; Search time 1435.66 Seconds
(without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579A-18

Perfect score: 28

Sequence: 1 aaatggtacagatgatactctgctt 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estlm:*
3: em_estln:*
4: em_estlm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.6	77.1	481	10	BE059008 sn23h02.y
2	20.2	72.1	600	13	BM078736 MEST123-F
3	20	71.4	495	14	W95055 2h48c01.s1
4	20	71.4	624	10	AV717903 AV717903
5	20	71.4	841	13	BI952375 BI952375
6	20	71.4	878	13	BI906578 BI906578

Result No.	Score	Query Match	Length	ID	Description
7	20	71.4	908	17	CNS07701
8	20	71.4	1051	14	BO940394
9	19.2	68.6	453	17	AZ990219
10	19.2	68.6	457	10	AM942444
11	19.2	68.6	460	17	PT013M03R
12	19.2	68.6	460	10	AM942444
13	19.2	68.6	460	10	AM942444
14	19.2	68.6	460	10	AM942444
15	19.2	68.6	460	10	AM942444
16	19.2	68.6	460	10	AM942444
17	19.2	68.6	460	10	AM942444
18	19.2	68.6	460	10	AM942444
19	19.2	68.6	460	10	AM942444
20	19.2	68.6	460	10	AM942444
21	19.2	68.6	460	10	AM942444
22	19.2	68.6	460	10	AM942444
23	19.2	68.6	460	10	AM942444
24	19.2	68.6	460	10	AM942444
25	19.2	68.6	460	10	AM942444
26	19.2	68.6	460	10	AM942444
27	19.2	68.6	460	10	AM942444
28	19.2	68.6	460	10	AM942444
29	19.2	68.6	460	10	AM942444
30	19.2	68.6	460	10	AM942444
31	19.2	68.6	460	10	AM942444
32	19.2	68.6	460	10	AM942444
33	19.2	68.6	460	10	AM942444
34	19.2	68.6	460	10	AM942444
35	19.2	68.6	460	10	AM942444
36	19.2	68.6	460	10	AM942444
37	19.2	68.6	460	10	AM942444
38	19.2	68.6	460	10	AM942444
39	19.2	68.6	460	10	AM942444
40	19.2	68.6	460	10	AM942444
41	19.2	68.6	460	10	AM942444
42	19.2	68.6	460	10	AM942444
43	19.2	68.6	460	10	AM942444
44	19.2	68.6	460	10	AM942444
45	19.2	68.6	460	10	AM942444

ALIGNMENTS

RESULT 1
LOCUS BE059008/c
DEFINITION sn23h02.y1 Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE 1D:
Gm-c1016-12364 5' similar to SW:ROK_HUMAN 007244 HETEROGENEOUS
NUCLEAR RIBONUCLEOPROTEIN K ; mRNA sequence.

ACCESSION BE059008.1 GI:8403374

VERSION
KEYWORDS
SOURCE

ORGANISM

soybean.
Glycine max

REFERENCE
AUTHORS
Shoemaker, R., Keim, P., Vockin, L., Eppel, J., Corry, V., Khanna, A., Bolla, B., Merritt, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE

JOURNAL

COMMENT

Public Soybean EST Project

Public Soybean EST Project

Public Soybean EST Project

Public Soybean EST Project

Public Soybean EST Project

Public Soybean EST Project

Public Soybean EST Project

Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: ccutefresgen.com
 Insert length: 1791 Std Error: 0.00
 Seq primer: -40RP from Gibco
 High quality sequence stop: 423.

FEATURES

source

Location/Qualifiers

1..481
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1016-12364"
 /clone.lib="Gm-c1016"
 /tissue_type="Immature flowers of field grown plants"
 /lab_host="X110-Gold"
 /note="vector: pBluescript II XR; Site_1: EcoRI; Site_2:
 XhoI; This cDNA library was constructed from mRNA isolated
 from immature flowers of field grown plants. The cDNA
 library was prepared using the Stratagene pBluescript II
 XR library construction kit. Complementary DNA was
 synthesized from mRNA using a primer consisting of a poly
 (dT) sequence with a XhoI restriction site. EcoRI adaptors
 were ligated to the blunt-ended cDNA fragments followed by
 XhoI digestion. The cDNA fragments were directionally
 cloned into the EcoRI-XhoI restriction site of the
 pBluescript vector. The ligated cDNA fragments were
 transformed into X110-Gold host cells. This library was
 constructed by Dr. Randy Shoemaker and Dr. John
 Ertelding."

BASE COUNT 141 a 116 c 88 g 136 t
 ORIGIN

Query Match 77.1%; Score 21.6; DB 10; Length 481;
 Best Local Similarity 85.7%; Pred. No. 27;

Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AATTGGCTACAGATGATCCTTCCTT 28

Db 203 AAGTTGGCAAAAGATGATCCTTACTT 176

RESULT 2

BM078736

LOCUS 600 bp mRNA linear EST 14-NOV-2001
 DEFINITION MEST123-F06.T3 ISUM4-TN Zea mays cDNA clone MEST123-F06 3', mRNA

ACCESSION

BM078736

VERSION

BM078736.1

WORDS

EST.

JRCCE

ORGANISM

Zea mays.

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:

Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: PACC

clade: Panicoideae: Andropogoneae: Zea.

1 (bases 1 to 600)

Olu.F., Cui.F., Guo.L., Ashlock,D.A., Men.T.J. and Schnable,P.S.

Expressed Sequence Tags from B73 Maize seedlings and silks

Unpublished (2001)

Contact: Patrick S. Schnable

Schnable Laboratory

Iowa State University

4405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA

Tel: 515-294-0975

Fax: 515-294-2299

Email: schnable@iastate.edu

Individual basecall and confidence value were assigned using the

Phred software.

(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b

rt>). Overall sequence quality assessment and vector trimming were

conducted using the Lucy software (<http://www.ligr.org/softlab/>).

Lucy parameters were set to ensure an overall trimmed quality of

97.5% or better without any vector fragments in the chosen

high-quality region of each sequence. Low-quality bases between the
 poly-T and the high-quality region were replaced with N's to serve
 as spacers.
 PCR Primers
 FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
 CTA TAC)
 BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC
 TAA AG)
 Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES

source

Location/Qualifiers

1..600
 /organism="Zea mays"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone="MEST123-F06"
 /clone.lib="ISUM4-TN"
 /tissue_type="Seedling and silk"
 /lab_host="DH10B"
 /note="vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
 ds-cDNA molecules were generated as follows. First-strand
 cDNA was prepared from oligo-dT selected mRNA by priming
 with a Noli oligo-dT primer (5'
 AACTGAGAGATTGGCGCGCAGGAATTTTTTTTTTTT). The
 resulting DNA:RNA hybrid was treated with RNase H and used
 as a template for DNA PolI-catalyzed second strand
 synthesis. After the addition of EcoRI adaptors, the
 ds-cDNAs were digested with NotI and size-selected. The
 resulting molecules were directionally cloned into the
 EcoRI and NotI sites of the pT73PAC vector. The library
 then went through one round of normalization to 10⁶ value
 of 5 based on the methods of Marcelo Bento Soares (Genome
 Research 6: 791-806, 1996)."

BASE COUNT 164 a 151 c 101 g 184 t
 ORIGIN

Query Match 72.1%; Score 20.2; DB 13; Length 600;
 Best Local Similarity 88.0%; Pred. No. 1.3e+02;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 TTGGGTACAGATGATCCTTCCTT 28

Db 155 TTGGGTCAAAAGATGATCCTTCCTT 179

RESULT 3

W95055

LOCUS 495 bp mRNA linear EST 02-FEB-1997
 DEFINITION zh48c01.s1 Soares_fetal_liver_spleen_INFLS.S1 Homo sapiens cDNA

ACCESSION

W95055

VERSION

W95055.1

WORDS

EST.

SOURCE

human.

Homo sapiens

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:

Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.

1 (bases 1 to 495)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chapell,B.,

Chisoso,S., Dietrich,N., Dubuque,T., Favella,A., Gish,W., Hawkins

,M., Hultman,M., Kucaba,T., Laey,M., Le,M., Le,N., Mardis,E., Moore

,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,

Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,

Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available royalty-free through LUNL; contact the

and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see

<http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Ming R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://heat.pw.usda.gov/ggpages/bgn/31/cover.html>)

BASE COUNT 167 a 232 c 262 g 180 t

Query Match Best Local Similarity 82.1%; Score 20; DB 13; Length 841; Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 AATTGGCTACAGATGATACCTTCGTT 28
DB 535 AATGGGGAAGATGATGATCTTCGTT 508

SUIT 6
LOCUS B1906578 878 bp mRNA linear EST 16-OCT-2001
DEFINITION 603064215F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5213378 5',
ACCESSION B1906578
VERSION B1906578.1 GI:16169320
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 878)
NIH-MGC <http://mhc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
plate: L1AM1535 row: n column: 03
High quality sequence slope: 787.
Location/Qualifiers
1..878
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_11b="NIH_MGC_118"
/issue_type="Leukocyte"
/lab_host="DH10B"
/note="Vector: PCWV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source: leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH-MGC Library."

BASE COUNT 273 a 181 c 168 g 256 t

ORIGIN

Query Match Best Local Similarity 82.1%; Score 20; DB 13; Length 878; Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 AATTGGGTACAGATGATACCTTCGTT 28

DB 584 AACTGGATACAGATGATACCTTCATT 557

RESULT 7
LOCUS CNS077UI 908 bp DNA linear GSS 08-JUL-2001
DEFINITION T7 end of clone BB0AA014F11 of library BB0A from strain CBS 4732 of *Pichia angusta*, genomic survey sequence.
ACCESSION AL433168
VERSION AL433168.1 GI:12216582
KEYWORDS GSS.
SOURCE *Pichia angusta*.
ORGANISM *Pichia angusta*.
Fungal; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; *Pichia*.
1 (bases 1 to 908)
Souciell,J.L., Aigle,M., Arligueneve,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brolhier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durans,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEMS Lett. 487 (1), 3-12 (2000)

REFERENCE
AUTHORS Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Arligueneve,F. and Dujon,B.
TITLE Genomic exploration of the hemiascomycetous yeasts: 13. *Pichia angusta*
FEMS Lett. 487 (1), 76-81 (2000)
MEDLINE 20584723
PUBMED 11152888
JOURNAL 3 (bases 1 to 908)
REFERENCE
AUTHORS
TITLE Genoscope.
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *varium*, *Saccharomyces* *exiguus*, *Saccharomyces servazii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces* *lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia* *angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbophilola*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
Location/Qualifiers
1..908
/organism="Pichia angusta"
/strain="CBS 4732"
/db_xref="taxon:4905"
/clone_11b="BB0AA014F11"
/clone_11b="BB0AA"
/note="end: T7"
complement(38..5847)
/note="similar to *Saccharomyces cerevisiae* ORF YEL055c [PO15: DNA polymerase V 1]"
/evidence="not experimental"

BASE COUNT 220 a 181 c 196 g 310 t

ORIGIN

Query Match Best Local Similarity 82.1%; Score 20; DB 17; Length 908; Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 AATTGGGTACAGATGATACCTTCGTT 28

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydriidae; Drosophilidae; Drosophila.
1 (bases 1 to 457)
Harvey, D., Brokslein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S., and Rubin, G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
Other_ESTs: LD17235.5prtime
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST/estfruitfly.berkeley.edu>
Based upon the presence of a xhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed. hit
genomic A6003796: Drosophila melanogaster genomic scaffold
1420001386047 section 6 of 52, complete sequence.: 02/23/2001
Plate: LD.172 row: C column: 11
High quality sequence stop: 377.

FEATURES
source
1..457
Location/Qualifiers
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="LD17235"
/clone_1lb="LD Drosophila melanogaster embryo Bluescript"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
/note="Organ: embryo; Vector: Bluescript SK; Site_1: EcoRI
; Site_2: XhoI; Constructed using Stratagene ZAP-cDNA
Synthesis kit. Oligo dt-primed and directionally cloned at
EcoRI and XhoI in Bluescript SK(+/-)"
BASE COUNT
101 a 121 c 127 g 108 t
ORIGIN

Query Match 68.6%; Score 19.2; DB 10; Length 457;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 TTGGCTACAGATGATACCTTCCT 27
1 ||||| ||||| ||||| ||||| |||||
DB 78 TGGGGTTCAAGATGATACCATCCT 101

RESULT 11
PT013M03R 460 bp DNA linear GSS 13-JUL-2001
OCUS
FINITION
Paramecium tetraurelia sequence R13G02r of the end of plasmid
PT013M03, genomic survey sequence.
ACCESSION
AL446163.1 GI:11123054
KEYWORDS
GSS.
SOURCE
Paramecium tetraurelia.
ORGANISM
Paramecium tetraurelia.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Penicillulida;
Paramacium.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

1 (bases 1 to 460)
Keller, A.M. and Cohen, J.
An indexed genomic library for Paramecium complementation cloning
J. Eukaryot. Microbiol. 47 (1), 1-6 (2000)
20114709
10651287
2 (bases 1 to 460)
Dassen, P., Zagulski, M., Gromadka, R., Plattner, H., Kismehl, R.,
Meyer, E., Betenheimer, M., Schultz, J.E., Linder, D., Pearlman, R.E.,
Kung, C., Forney, J., Satir, B.H., Van Houten, J.L., Keller, A.M.,
Froisard, M., Sperling, L. and Cohen, J.
Paramecium genome survey: a pilot project
Trends Genet. 17 (6), 306-308 (2001)
TITLE
JOURNAL
MEDLINE
PUBMED
FBI MED

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

3 (bases 1 to 460)
Wong, L. and Pearlman, R.E.
Random sequencing of the Paramecium macronuclear genome
Unpublished
Core Molecular Biology Facility, York University, 4700 Keele St.,
Toronto, Canada M3J 1P3
4 (bases 1 to 460)
Cohen, J. and Sperling, L.
Direct Submission
Submitted (01-NOV-2000) Paramecium Genome Survey Project, Centre de
Genetique Moleculaire, Centre National de la Recherche
Scientifique, 91198 Gif-sur-Yvette, France. E-mail:
sperling@cgm.cnrs-gif.fr
The present survey of the Paramecium tetraurelia macronuclear
genome consists of end sequences of a library of random 4-12 kb
fragments obtained by Sau3A partial digestion of macronuclear DNA
cloned in the BamHI site of pBS1KS-. See [4].
Genes are predicted from matches to other sequences. For more
information about this sequence or the Paramecium Project, see
<http://paramecium.cgm.cnrs-gif.fr>.

FEATURES
source
1..460
Location/Qualifiers
/organism="Paramecium tetraurelia"
/macronuclear
/strain="stock d4-2"
/db_xref="taxon:5888"
BASE COUNT
165 a 62 c 63 g 170 t
ORIGIN

Query Match 68.6%; Score 19.2; DB 17; Length 460;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AATTGGTACAGATGATACCTTC 25
1 ||||| ||||| ||||| ||||| |||||
DB 102 AATTGGATTCATATGATACCTTC 125

RESULT 12
BB171446/c 245 bp mRNA linear EST 29-JUN-2000
LOCUS
BB171446 RIKEN full-length enriched, adult male hypohalamus Mus
musculus cDNA clone A230028C13 3', mRNA sequence.
ACCESSION
BB171446
VERSION
BB171446.1 GI:8830529
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 245)
Konno, H., Aizawa, K., Akahira, S., Akiyama, I., Arakawa, T., Carninci,
P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, U., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata,
Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomioka, N., Toya,
T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamanaoka, I.,
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino,
M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitama-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.go.jp

FEATURES	Location/Qualifiers
source	1. .245

**BASF: COUNT
ORIGIN**

Matches

Db 74 A

ORGANISM

COMMENT

FEATURES

ORIGIN

Matches

Db 141

1
2
3
4
5
6
7
8
9

SOURCE

AUTHORS

TITLE

Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. *Genome Res.* 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES	Location/Qualifiers
source	1. .330

/note="Site_1": Sall; Site_2 BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research group in Riken genomic Sciences Center and Genome Science laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 15' GAGCAGAGCAACGATCCAGACACTCTCTTTTTTTTTTNN 3', cDNA was prepared by using trehalase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence 15' GAGCAGACACTCTCGAGTTAAATTAATTCACCCCCCCCCCCCC 3'. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda

BASE COUNT	72 a	53 c	51 g	154 t
ORIGIN				

Query Match	67.98;	Score 19;	DB 10;	Length 330;
Best Local Similarity	81.58;	Pred. No. 3.5e+02;		
Matches 22;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

```

OY      1 AAATGGCTACAGATGATACCTTGT 27
        ||| ||| ||||| || ||||| ||
DB      96 AAATGGCTACAGTGTACCTTGT 70

```

	JULY 15	
	.254027/c	
LOCUS	AM254027	404 bp
DEFINITION	UI-R-Bj0-aec-c-10-0-UI.s1 UI-R-Bj0 Rattus norvegicus cDNA clone	mRNA linear EST 17-DEC-1999
ACCESSION	AM254027	
VERSION	AM254027.1	GI:6597618
KEYWORDS	EST.	
SOURCE	Norway rat,	
ORGANISM	Rattus norvegicus	

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 404)	Ronaldo, M.F., Lennon, G. and Soares, M.B.	Normalization and subtraction: two approaches to facilitate gene

COMMENT

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250

Fax: 319 335 9565
 Email: mscares@blue.weeg.uiowa.edu
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized AV canal at 15 dpb library cDNA library preparation: M.H. Scores Lab clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-82,
 >AT-rich#Low_complexity 363-395, >AT-rich#Low_complexity
 Seq primer: M13 Forward
 SOLTA=yes.

FEATURES	Location/Qualifiers
source	1. .404

lab_host"DH10B (Life Technologies)"
/not/Vector: PT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The *ut-R-30*
library is a subcloned library derived from the *ut-R-AM1*,
and *ut-R-AG1*, *ut-R-AC1*, *ut-R-AD1*, *ut-R-AE1*, *ut-R-AF1*, and
ut-R-AG1 libraries. These libraries represent tissues from
rat atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal
at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV
canal at 13 dpc, and ventricle at 13 dpc. The tag is a
string of 3-6 nucleotides present between the Not I site
and the *oligo* tag track. The library was constructed as
described by Bonaldo, Lennon and Soares, Genome Research
6: 791-806, 1996.

TAG_TISSUE=AV canal at 15 dpc
TAG_SEQ=GAAGG"

BASE COUNT	140 a	62 c	72 g	130 t
ORIGIN				

Query Match	67.9%	Score 19;	DB 10;	Length 404;
Best Local Similarity	81.5%;	Pred. No. 3.8e+02;		
Matches 22; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

oy 1 AAATGGGTACAAGATGATACCTTCGT 27
||| ||||| ||| ||
Db 360 AAGTATTTCACAGATGATACCTTAGT 334

Search completed: December 10, 2002, 22:49:46
Job time : 1441.66 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:03:28 ; Search time 182.547 Seconds
(without alignments)
345.422 Million cell updates/sec

Title: US-09-865-579A-18

Perfect score: 28
Sequence: 1 aaattggtacaaagatgatacttcgtcgt 28

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: N_Geneseq_101002:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
25: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	28	24	ABK85918
2	28	100.0	1789	16	AAOT04536
3	28	100.0	2007	13	AAQ28599
4	28	100.0	2007	17	AAAT28568
5	28	100.0	2007	19	AAV68337
6	28	100.0	2007	22	ABA76993
7	28	100.0	2028	24	ABN92247
8	28	100.0	2110	14	AAQ35213
9	28	100.0	2322	13	AAQ25905

10	28	100.0	2455	16	AAOT04538	Staphylococcus aur
11	28	100.0	2456	22	AAH01187	Staphylococcus aur
12	20	71.4	3800	24	ABO70885	Listeria monocytog
13	18.6	66.4	462	16	AAIT20797	Human gene signalu
14	18.4	65.7	381	22	AAE65394	Novel Human polynu
15	18.4	65.7	563	22	AAH10449	Human cDNA clone (
16	18.4	65.7	845	20	AAK61426	DNA encoding a hum
17	18.4	65.7	2182	22	AAH15656	Human cDNA sequenc
18	18.4	65.7	6495	22	AA540553	DNA encoding human
19	18.4	65.7	6495	22	AA106441	Human reproductive
20	18.4	65.7	12100	22	AA540550	DNA encoding human
21	18.4	65.7	12100	22	AA106438	Human reproductive
22	18.4	65.7	12100	22	AAK69502	Human immune/haema
23	18.4	65.7	12100	22	AAK72028	Human immune/haema
24	18.4	65.7	12100	22	AAK72706	Human immune/haema
25	18.4	65.7	14254	22	ABA17489	Human nervous syst
26	18	64.3	232	24	ABN93784	Gene #262 used to
27	18	64.3	232	24	ABN93784	Colon adenocarcino
28	18	64.3	277	24	ABK45636	cDNA encoding colo
29	18	64.3	492	22	AA119664	Human breast cance
30	18	64.3	732	21	AAA97370	Human colorectal c
31	18	64.3	1079	22	AA560801	Human cancer agent
32	18	64.3	2500	23	ABL16703	Drosophila melanog
33	18	64.3	12216	23	ABL16702	Drosophila melanog
34	17.8	63.6	1256	23	ABL13891	Drosophila melanog
35	17.8	63.6	3400	23	ABL13890	Drosophila melanog
36	17.8	63.6	10109	23	ABL14568	Drosophila melanog
37	17.6	62.9	452	18	AAV20187	Probe (88) for mic
38	17.6	62.9	452	18	AAV4893	Staphylococcus aur
39	17.6	62.9	683	23	ABL13207	Drosophila melanog
40	17.6	62.9	1029	21	AA54437	Arabidopsis thalia
41	17.6	62.9	1309	21	AA542970	Arabidopsis thalia
42	17.6	62.9	1309	21	AA54439	Arabidopsis thalia
43	17.6	62.9	2780	23	ABL13292	Drosophila melanog
44	17.6	62.9	3085	23	ABL13206	Drosophila melanog
45	17.6	62.9	4329	23	AA51367	Enterococcus faeca

ALIGNMENTS

RESULT 1
ID ABR85918 standard; DNA: 28 BP.
AC ABR85918;
XX
XX 16-AUG-2002 (first entry)
DT
XX
DE Methicillin resistant Staphylococcus aureus detection primer #18.
XX
XX
KM Methicillin resistant Staphylococcus Aureus; MRSA; primer: ss;
KM meca; probe.
XX
OS Staphylococcus aureus.
XX
PN EPI160333-A2.
XX
PD 05-DEC-2001.
XX
PF 29-MAY-2001; 2001EP-0112100.
XX
PR 29-MAY-2000; 2000JP-0163149.
XX
PR 09-JUN-2000; 2000JP-0179394.
XX
XX (TOY) TOSOH CORP.
PA Taya T, Ishiguro T, Saito J;
PI WPI; 2002-395832/43.
XX
XX New oligonucleotide specific for the meca methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related

PT mRNA -
PS Claim 5; Page 19; 28pp; English.

XX This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the mecA gene (associated with methicillin resistance in
CC *Staphylococcus aureus*) or its derivative RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the mecA gene as template. Also disclosed is a detection
CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant *S. aureus* in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the mecA gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.

XX Sequence 28 BP; 9 A; 4 C; 6 G; 9 T; 0 other;

Query Match 100.0%; Score 28; DB 24; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.0022; Mismatches 0; Gaps 0;

Matches 28; Conservative 0; Indels 0; Gaps 0;
OY 1 AAATTGGGTACAGATGATGATCTTCGTT 28
DB 1 AAATTGGGTACAGATGATGATCTTCGTT 28

RESULT 2
AAAT04536
ID AAAT04536 standard; cDNA to mRNA; 1789 BP.

XX AAT04536;

XX 11-APR-1996 (first entry)

XX *Staphylococcus aureus* 'meca' protein coding sequence.

XX methicillin-resistant *Staphylococcus aureus*; MRSA; 'meca' protein;
XX antibiotic resistance; ds.

XX *Staphylococcus aureus*.

Key Location/Qualifiers

CDS 1..1608
/*tag= a
/product= 'mec_A'-protein

JP07209294-A.

11-AUG-1995.

10-JAN-1994; 94JP-0012226.

10-JAN-1994; 94JP-0012226.

(DENK-) DENKA SEIKEN KK.

(KAWA/) KAWANO M.

(MITU) MITSUBISHI CHEM CORP.

WPI; 1995-313917/41.

P-PSDB; AAR80035.

New 'mec A' protein and DNA encoding it - used for the detection of
methicillin-resistant *Staphylococcus aureus*

PS Claim 5; Page 11-13; 15pp; Japanese.

XX The present sequence codes for the 'mec A' protein which controls
CC methicillin resistance in methicillin-resistant *Staph. aureus*. The
CC 'mec A' protein (mol. wt. 40000) is useful for preparation of
CC an antiserum specific for MRSA, thereby allowing methicillin-resistant
CC and methicillin-sensitive strains to be distinguished. The coding
CC sequence was obtained by PCR amplification of the mec A sequence
CC (see AAAT04536) using primers AAAT04537 and AAAT04539.
CC N.B. in the sequence listing of the patent specification, the
CC sequence length is stated to be 1785 bp.

XX Sequence 1789 BP; 735 A; 263 C; 302 G; 489 T; 0 other;

Query Match 100.0%; Score 28; DB 16; Length 1789;

Best Local Similarity 100.0%; Pred. No. 0.0036; Mismatches 0; Gaps 0;

Matches 28; Conservative 0; Indels 0; Gaps 0;
OY 1 AAATTGGGTACAGATGATGATCTTCGTT 28
DB 203 AAATTGGGTACAGATGATGATCTTCGTT 230

RESULT 3
AAQ28599

ID AAQ28599 standard; DNA; 2007 BP.

XX AAQ28599;

XX 19-FEB-1993 (first entry)

XX Encodes penicillin binding protein PBP2A-27R.

XX penicillin; antibiotic; bacteria; methicillin; *staphylococci*;
XX soluble; chelating peptide; MRS infection; methicillin resistant;
XX strain.

XX *Staphylococcus aureus* strain 27R.

Key Location/Qualifiers

CDS 1..2007

/*tag= a

EP505151-A.

23-SEP-1992.

18-MAR-1992; 92EP-0302298.

19-MAR-1991; 91US-0672704.

(ELIL) LILLY & CO ELI.

Blaszczak LC, Skatrud PL, Smith MC, Wu CYE;

WPI; 1992-318034/39.

Polynucleotide cpd. encoding PBP 2A-27R protein or its deriv. -
contains PBP isolated from *Staphylococcus aureus* and is used to
treat methicillin resistant *staphylococci*

Disclosure; Page 14; 101pp; English.

XX This sequence encodes a PBP2a penicillin binding protein isolated
CC from *S. aureus* strain 27R. A cDNA library was constructed from
CC *S. aureus* DNA in lambda phage EMBL3. Packaging extracts from this
CC were used to infect *E. coli* Cj236. Plaques were screened for the
CC presence of the mecA-27R gene by a probe produced by PCR amplification
CC of the mecA gene using primers Q28600.1. Positive plaques were purified
CC and digested with HindIII, and this fragment digested with XbaI and
CC cloned into M13amp8 and M13amp19 for sequencing.

XX Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;

Query Match 100.0%; Score 28; DB 13; Length 2007;
Best Local Similarity 100.0%; Pred. NO. 0.0037;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AATATGGGTACAGATGATACCTTGTT 28
|||||
609 AATATGGGTACAGATGATACCTTGTT 636

RESULT 4
AAT28568
AAT28568 standard; DNA: 2007 BP.
AAT28568:
01-APR-1997 (first entry)
Bacterial antibiotic resistance gene, mecA, probe.
Detection: probe; amplification primer; bacterial pathogen; pneumonia;
Escherichia coli; *Klebsiella pneumoniae*; *Pseudomonas aeruginosa*;
Proteus mirabilis; *Streptococcus pneumoniae*; *Staphylococcus aureus*;
Staphylococcus epidermidis; *Enterococcus faecalis*; respiratory tract;
Staphylococcus saprophyticus; *Streptococcus pyogenes*; urinary tract;
Haemophilus influenzae; *Moraxella catarrhalis*; septicemia; meningitis;
infection; intra-abdominal infection; skin infection;
bacterial resistance; beta-lactam antibiotic; ds.
Synthetic.
WO9608582-A2.
21-MAR-1996.
12-SEP-1995; 95WO-CA00528.
12-SEP-1994; 94US-0304732.
(BERG/) BERGERON M. C.
(OUEL/) OUELLETTE M.
(ROY/) ROY P. H.
Bergeron MG, Ouellette M, Roy PH;
WPI, 1996-179953/18.
Method for the detection of bacterial species using probes and
primers - allows detection and quantification of antibiotic
resistant bacteria in patients, the environment and food
Claim 91; Page 144-145; 216pp; English.

The sequences given in AAT28560-76 represent fragments derived from
bacterial antibiotic resistance genes which were used as probes in the
method of the invention for the detection of bacterial species in a
sample. The method of the invention comprises using probes and/or
amplification primers which are specific, ubiquitous and sensitive for
determining the presence and/or amount of nucleic acids from selected
bacterial species in any sample, where the bacterial nucleic acid
comprises a selected target region hybridisable with the probes or
primers. The method comprises contacting the sample with the probes
or primers and detecting the presence and/or amount of hybridised
primers or amplification products as and indication of the presence
and/or amount of the bacterial species. This method may be used to
detect commonly encountered bacterial pathogens, e.g. *Escherichia coli*,
Klebsiella pneumoniae, *Pseudomonas aeruginosa*, *Proteus mirabilis*,
Streptococcus pneumoniae, *Staphylococcus aureus*, *Staphylococcus*
epidermidis, *Enterococcus faecalis*, *Staphylococcus saprophyticus*,
Streptococcus pyogenes, *Haemophilus influenzae* and *Moraxella*
catarrhalis. These bacterial species are associated with approx. 90% of
urinary tract infections and with a high percentage of other severe
infections including septicemia, meningitis, pneumonia, intra-abdominal

	infections , skin infections and other severe respiratory tract
CC	infections . The method may also be used to evaluate a bacterial
CC	resistance to beta- lactam antibiotics.
XX	
SQ	Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
OY	1 AAATGGGTACAGATGATTACTTCTTGTT 28
Dd	608 AAAATGGGTACAGATGATTACTTCTTGTT 635
RESULT 5	
ID	AAV68337 standard; DNA: 2007 BP.
XX AC	AAV68337;
XX DT	21-JUN-1999 (first entry)
DE	Penicillin binding protein PBP2A meca-27R gene of S. aureus 27R.
XX	
KW	Penicillin binding protein: PBP2A-27A; meca-27R gene;
XX KM	methicillin resistance; antibiotic; assay; purification; ss.
XX OS	Staphylococcus aureus.
PN	EP85578-A2.
PD	04-NOV-1998 .
PE	18-MAR-1992; 92EP-0302298.
PR	19-MAR-1991; 91US-0672704.
PA	(ELIL) LILLY & CO ELI.
PI	Biaszczak LC, Skatrud PL, Smith WC, Wu CE;
DR	WPI: 1998-559443/48. P-PADB: AAW81149.
PT	New Staphylococcus aureus soluble penicillin-binding proteins and their derivatives - useful for screening for compounds effective against methicillin resistant organisms
PS	Disclosure: Page 14-16; 97pp; English.
XX	This meca-27R gene encodes penicillin binding protein 2A (PBP2A-27R) responsible for the methicillin resistance of Staphylococcus aureus strain 27R. The invention provides new PBPs of formula SP-L-PBP2As, where: SP is 0 or a signal peptide (preferably from the amcC, ompA or beta-lactamase gene product); L is Met-Val or a compound of formula Met-Gly-C(=Pro)n-PBP2As), were CP = 0 or a chelating peptide (see CC AAM8151-58) of formula (His)x-(A)y(His)z and A-an amino acid, x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above polypeptide where each monomer unit is the same or different: Pro is proline, n = 0 or 1; and PBP2As is soluble PBP2A-27R protein (see CC AAW8159-62). Also claimed are polynucleotides encoding specific soluble PBP2A compounds. The new PBP2A-27R proteins are useful for assaying for agents useful as antibiotics against methicillin resistant Staphylococcus strains by creating a kinetically inert complex between a support-immobilised transition ion and a modified soluble PBP2A protein comprising a chelating agent, which screens for agents which bind to PBP2A proteins (disclosed). Soluble forms of PBP2A-27R protein facilitate crystallisation as they lack their transmembrane association region, and so are useful for x-ray crystallography studies of the protein, assisting in the design of antibiotic compounds against methicillin resistant staphylococcus strains (disclosed). The chelating peptide operably linked to the

CC BP2A-27R proteins is useful for purifying PBPs.
XX
SQ Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;

Query Match 100.0%; Score 28; DB 19; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAATGGGTACAGATGATACCTTCGTT 28
|||||
DB 609 AAATGGGTACAGATGATACCTTCGTT 636

RESULT 6
ABA76993
ID ABA76993 standard; DNA: 2007 BP.

AC ABA76993;

DT 28-JAN-2002 (first entry)

X Antibiotic resistance detection polynucleotide SEQ ID NO 169.

KM Detection: bacterial species; animal; food; environment;
KW antibiotic resistance; ds.

OS Unidentified.

PN NZ501596-A.

PD 29-JUN-2001.

PF 12-SEP-1995; 95NZ-0501596.

PR 12-SEP-1995; 95NZ-0501596.

PA (IDI-) IDI INFECTION DIAGNOSTIC INC.

PI Bergeron MG, Ouellette M, Roy PH;

DR WPI: 2001-615034/71.

PT Method for detecting target bacterial species in a sample, comprises
PT detecting the presence or amount of bacterial nucleic acid amplified by
PT a primer derived from bacterial DNA, specific for the target bacterial
PT species -

PS Claim 16: Page 159-160; 168pp; English.

XX The invention relates to detecting target bacterial species suspected to
be present in a sample, comprising contacting nucleic acids of target
bacterial species with an amplification primer pair derived from a
bacterial DNA fragment (ABA76825-ABA76861) specific for the target
bacterial species but ubiquitous for different strains, amplifying the
nucleic acid and detecting the presence or amount of an amplified
sequence as an indication of the presence or amount of the target
bacterial species. The invention includes primers and probes
(ABA76862-ABA76984) against the target bacterial species, especially
E.coli, K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae,
S.aureus, S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes,
H.influenzae, M.catalhalis and/or group A Streptococci producing
exotoxin A gene spe A, suspected to be present in a sample which is
obtained from human patients, animals, environment or food, and which
consists of one or more bacterial colonies. Oligonucleotide
probes and primers complementary to the bacterial genes encoding
resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aadB,
aac(1), aac(2), aac(3), aac(4), mecA, vanA, vanH, vanX, satA, aac-aphD, vat,
vga, msrA, sul and/or int (ABA76985-ABA77001) are also useful to identify
commonly encountered and clinically important resistance genes. The
invention provides a rapid method of bacterial identification that can be
achieved, which reduces the time currently required for the
identification of pathogens in the clinical laboratory.

SQ Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;

Query Match 100.0%; Score 28; DB 22; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAATGGGTACAGATGATACCTTCGTT 28
|||||
DB 608 AAATGGGTACAGATGATACCTTCGTT 635

RESULT 7
ABN92247
ID ABN92247 standard; DNA: 2028 BP.

AC ABN92247;

DT 24-JUL-2002 (first entry)

DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1710.

KM Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW antibacterial; gene therapy; gene; ds.

OS Staphylococcus epidermidis.

PN US6380370-B1.

PD 30-APR-2002.

PF 13-AUG-1998; 98US-0134001.

PR 14-AUG-1997; 97US-055779P.

PR 08-NOV-1997; 97US-064964P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Doucelte-Stamm LA, Bush D;

DR WPI: 2002-381255/41.

DR P-PSDB; ABP39702.

PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
PT polypeptide, useful for diagnosing and treating bacterial infections -
PT disclosure; SEQ ID 1710; 267pp; English.

XX ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC antibacterial activity and can be used in gene therapy. The sequences
CC can also be used in the diagnosis and treatment of bacterial infections,
CC particularly S. epidermidis infections. The sequences can be used to
CC screen for compounds able to interfere with the S. epidermidis life
CC cycle or inhibit S. epidermidis infection.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site.

SQ Sequence 2028 BP; 861 A; 273 C; 346 G; 547 T; 1 other;

Query Match 100.0%; Score 28; DB 24; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAATGGGTACAGATGATACCTTCGTT 28
|||||
DB 630 AAATGGGTACAGATGATACCTTCGTT 657

RESULT 8
AA035213
ID AA035213 standard; DNA: 2110 BP.

```

XX AC AAQ35213;
XX DT 06-JUN-1993 (first entry)
XX DE Sequence of the mec A gene.
XX KW Methicillin-resistant staphylococci; detection; primer; PCR; ss.
XX OS Staphylococcus aureus.
XX FH Key
XX FT CDS
XX FT 105..2110
XX FT /*tag= a
XX PN EP527628-A.
XX PD 17-FEB-1993.
XX PS 10-AUG-1992; 92EP-0307307.
XX PR 13-AUG-1991; 91US-0744770.
XX PA (E.L.I.L.) LILLY & CO E.L.I.
XX P1 Skatrud PL, Unal S;
XX DR WPI; 1993-054352/07.
XX DR P-PSDB; AAR30845.
XX PT Detection of methicillin-resistant staphylococci - using
XX PT polymerase chain reaction method, and DNA primers, for rapid,
XX PT sensitive and accurate detection
XX PS Disclosure; pages 7-10; 16pp; English.
XX CC The inventors claim a method for detecting methicillin-resistant
XX CC staphylococcal infections which involves the use of the PCR primed
XX CC by fragments of the Staphylococcus meca gene. More specifically, the
XX CC initial primers used are nucleotides 141-160 and the inverse
XX CC complement of nucleotides 1929-1952 of the S. aureus meca gene. The
XX CC interior primers are nucleotides 568-593 and the inverse complement
XX CC of 1647-1670 of the S. aureus meca gene.
XX SQ Sequence 2110 BP; 896 A; 290 C; 350 G; 574 T; 0 other;
XX
XX Query Match 100.0%; Score 28; DB 14; Length 2110;
XX Best Local Similarity 100.0%; Pred. No. 0.0037;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAATTGGGTACAAAGATGATACCTTCGTT 28
DB 713 AAATTGGGTACAAAGATGATACCTTCGTT 740

```

```

XX PN JP04169200-A.
XX PD 17-JUN-1992.
XX PS 31-OCT-1990; 90JP-0296708.
XX PR 31-OCT-1990; 90JP-0296708.
XX PA (SHIO ) SHIONOGI & CO LTD.
XX DR WPI; 1992-253403/31.
XX PS 17-AUG-1992; 92EP-0307307.
XX PR 13-AUG-1991; 91US-0744770.
XX PA (E.L.I.L.) LILLY & CO E.L.I.
XX P1 Skatrud PL, Unal S;
XX DR WPI; 1993-054352/07.
XX DR P-PSDB; AAR30845.
XX PT Detection of methicillin-resistant staphylococci - using
XX PT polymerase chain reaction method, and DNA primers, for rapid,
XX PT sensitive and accurate detection
XX PS Disclosure; pages 7-10; 16pp; English.
XX CC The inventors claim a method for detecting methicillin-resistant
XX CC staphylococcal infections which involves the use of the PCR primed
XX CC by fragments of the Staphylococcus meca gene. More specifically, the
XX CC initial primers used are nucleotides 141-160 and the inverse
XX CC complement of nucleotides 1929-1952 of the S. aureus meca gene. The
XX CC interior primers are nucleotides 568-593 and the inverse complement
XX CC of 1647-1670 of the S. aureus meca gene.
XX SQ Sequence 2110 BP; 896 A; 290 C; 350 G; 574 T; 0 other;
XX
XX Query Match 100.0%; Score 28; DB 13; Length 2322;
XX Best Local Similarity 100.0%; Pred. No. 0.0038;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAATTGGGTACAAAGATGATACCTTCGTT 28
DB 608 AAATTGGGTACAAAGATGATACCTTCGTT 635

```

```

RESULT 10
AA04538
ID AA04538 standard; cDNA to mRNA; 2455 BP.
XX AC AA04538;
XX DT 11-APR-1996 (first entry)
XX DE Staphylococcus aureus meca protein coding sequence.
XX KW methicillin-resistant Staphylococcus aureus; MRSA; 'meca protein;
XX KW antibiotic resistance; ds.
XX OS Staphylococcus aureus.
XX FH Key
XX FT CDS
XX FT 134..2146
XX FT /*tag= a
XX FT /product= mec_A-protein
XX PN JP07209294-A.
XX PD 11-AUG-1995.
XX PS 10-JAN-1994; 94JP-0012226.
XX PR 10-JAN-1994; 94JP-0012226.
XX PA (DENK-) DENKA SEIKEN KK.
XX PA (KAWA/) KAWANO M.
XX PA (MITU ) MITSUBISHI CHEM CORP.
XX DR WPI; 1995-313917/41.
XX DR P-PSDB; AAR80036.
XX PT New 'mec A protein and DNA encoding it - used for the detection of
XX PT methicillin-resistant Staphylococcus aureus

```

PS Example 2; Page 8-10; 15pp; Japanese.
XX
CC The present sequence codes for the mec A protein. DNA coding for
CC the 'mec A' protein, which controls methicillin resistance in
CC methicillin-resistant Staph. aureus (MRSA), was obtained by PCR
CC amplification of the mec A sequence using primers AAT04537 and
CC AAT04539. The 'mec A' protein (mol. wt. 40000) is useful for
CC preparation of antiserum specific for MRSA, thereby allowing
CC methicillin-resistant and methicillin-sensitive strains to be
CC distinguished.
XX
SQ Sequence 2455 BP; 997 A; 344 C; 401 G; 713 T; 0 other;
Query Match 100.0%; Score 28; DB 16; Length 2455;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 A A A T T G G T A C A A G A T G A T A C C T T C G T T 28
DB 741 A A A T T G G T A C A A G A T G A T A C C T T C G T T 768
JUL 11
AAH01187
ID AAH01187 standard; DNA: 2456 BP.
XX
AC AAH01187;
XX
DT 24-JUL-2001 (first entry)
XX
DE Staphylococcus aureus nucleotide sequence SEQ ID NO:1178.
XX
KM Species specific; genus specific; family specific; probe; detection;
KM identification; algal; archaeal; bacterial; fungal; parasitical;
KM microorganism; diagnosis; translation elongation factor Tu; toxin;
KM translation elongation factor G; RecA recombinase; resistance;
KM catalytic subunit of proton-translocating ATPase; antimicrobial;
KM vaccine; primer; ds.
XX
OS Staphylococcus aureus.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000MO-CA01150.
XX
PR 28-SEP-1999; 99CA-2283458.
PR 19-MAY-2000; 2000CA-2307010.
PR
(INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
AX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
XX WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and
PT primers which can be used to identify and detect the presence of algal,
PT archaeal, bacterial, fungal and parasitical species in a test sample -
XX
PS Disclosure; Page 1048-1049; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal
CC and parasitical species, genus, family and group. A nucleic acid (1)

CC obtained using the method of the invention can be used for the universal
CC detection of any bacterium, fungus or parasite in a sample and for the
CC detection of at least one antimicrobial agent resistance gene or at
CC least one toxin gene. hexa nucleic acids are used for the specific and
CC ubiquitous detection and for identification of Streptococcus pneumoniae.
CC (1) can be used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Adenoviridae, Escherichia coli,
CC Corynebacterium sp., Enterobacteriaceae group, Streptococcus sp.,
CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC provides faster results than substrate specificity tests as results can
CC be determined in an hour and improved accuracy is also achieved.
CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
CC which are given in the exemplification of the present invention.
XX
SQ Sequence 2456 BP; 1001 A; 344 C; 396 G; 715 T; 0 other;
Query Match 100.0%; Score 28; DB 22; Length 2456;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 A A A T T G G T A C A A G A T G A T A C C T T C G T T 28
DB 748 A A A T T G G T A C A A G A T G A T A C C T T C G T T 775
RESULT 12
ID ABQ70885 standard; DNA: 3800 BP.
XX
AC ABQ70885;
XX
DT 29-AUG-2002 (first entry)
XX
DE Listeria monocytogenes 4b contig DNA sequence #827.
XX
KM Antibacterial; Listeria; food contamination; mutational analysis;
KM infection; ds.
XX
OS Listeria monocytogenes 4b.
XX
PN WO200228891-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001MO-FR03061.
XX
PR 04-OCT-2000; 2000FR-0012697.
PR
(INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Kunst F, Glaser P;
XX
XX WPI; 2002-332479/37.
XX
PT New genomic sequences from Listeria species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators -
XX
PS Claim 14; SEQ ID 3698; 180pp; French.
XX
XX The present invention relates to nucleic acid sequences
CC (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes
CC and primers for identification and/or detection of Listeria (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of
CC gene expression. Proteins encoded by the nucleic acid sequences can be
CC used to screen for compounds that modulate gene expression, replication
CC and pathogenicity of Listeria (potential therapeutic agents), also for
CC treating infections by Listeria, and are useful as immunogens in
CC anti-Listeria vaccines.
CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3800 BP; 1230 A; 768 C; 714 G; 1084 T; 4 other;

Query Match 71.4%; Score 20; DB 24; Length 3800;
Best Local Similarity 82.1%; Pred. No. 19;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 AAATTGGGTACAGATGATCTTCGTT 28
||| ||||| ||||| ||||| |||||
Db 2300 AAAATGGGTCCACAGCATGATCTTCGTT 2327

RESULT 13
AAT20797/c
ID AAT20797 standard; cDNA to mRNA; 462 BP.

XX AAT20797:
X 09-JUL-1996 (first entry)
DE Human gene signature HUMGS02045.

XX Gene signature: messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
XX cell typing; abnormal cell function; ss.

OS Homo sapiens.

XX W09514772-A1.

XX 01-JUN-1995.

XX 11-NOV-1994; 94WO-JP01916.

XX 12-NOV-1993; 93JP-0355504.

PA (MATS/) MATSUBARA K.
PA (OROB/) OKUBO K.

PI Matsubara K, Okubo K;

DR WPI; 1995-206931/27.

XX Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
XX tissues

AX Claim 1; Page 726; 2245pp; Japanese.

CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "Gis" sequences
CC given in AAT19001-T26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(r) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.

SQ Sequence 462 BP; 133 A; 82 C; 99 G; 137 T; 11 other;

Query Match 66.4%; Score 18.6; DB 16; Length 462;
Best Local Similarity 80.8%; Pred. No. 65;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 ATTGGGTACAGATGATCTTCGTT 28
||| ||||| ||||| ||||| |||||
Db 305 ATTGGGTACAGATGATCTTCGTT 280

RESULT 14
AAF65394
ID AAF65394 standard; cDNA; 381 BP.

XX AAF65394;

XX 09-APR-2001 (first entry)

DE Novel human polynucleotide, SEQ ID NO: 1150.

XX Human; cytostatic; gene therapy; colon cancer; prostate cancer;
KW breast cancer; lung cancer; cancer detection; ss.

OS Homo sapiens.

XX W0200102568-A2.

XX 11-JAN-2001.

XX 30-JUN-2000; 2000WO-US18374.

XX 02-JUL-1999; 99US-0142310.

XX 02-JUL-1999; 99US-0142311.

XX (CHIR) CHIRON CORP.

XX (HSE-) HSEQ INC.

PI Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J, Kassam A;
PI Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G, Drmanac R;
PI Cerkenjajkov R, Drmanac S, Dickson M, Labat I, Leshkowitz D;
PI Kita D, Garcia V, Jones LW, Strache-Grain B;

XX WPI; 2001-091805/10.

XX Library of polynucleotides for diagnosing a cancerous state of a
PT mammalian cell and detecting cancer, particularly of the colon or
PT prostate, comprises: 3351 human polynucleotide sequences -
XX
XX
XX Claim 9; Page 708-709; 1046pp; English.

XX The present sequence is one of 3351 sequences in a library of human
CC polynucleotides. The library is used to detect differentially expressed
CC genes correlated with a cancerous state of a mammalian cell and can
CC detect colon, prostate, breast and lung cancer. The library can be used
CC to produce probes for detection of mRNA and to produce additional copies
CC of the polynucleotides. The probes can be used for chromosome mapping of
CC the polynucleotide and for detection of transcription levels. Ribozymes
CC or antisense oligonucleotides can be generated. The polynucleotides and
CC their gene products are used as genetic or biochemical markers (e.g. in
CC blood or tissues) that will detect the earliest changes along the
CC carcinogenesis pathway and/or monitor the efficacy of therapies and
CC preventive interventions. The polynucleotides, polypeptides and
CC antibodies against them can be used in pharmaceutical compositions to
CC treat the cancers and proliferative disorders such as neoplasia,
CC dysplasia and hyperplasia.

SQ Sequence 381 BP; 119 A; 92 C; 78 G; 92 T; 0 other;

Query Match 65.7%; Score 18.4; DB 22; Length 381;
Best Local Similarity 78.6%; Pred. No. 79;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATCTTCGTT 28
||| ||||| ||||| ||||| |||||
Db 286 AAAATGGGTACAGATCTTAATTGTT 313

Search completed: December 10, 2002, 17:32:27
Job time : 185.347 secs

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RESULT 15
AAH10449/c
ID AAH10449 standard; cDNA: 563 BP.
XX
AC AAH10449;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (3'-primer) SEQ ID NO:7284.
XX
KW Human; primer: detection; diagnosis: antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 3: SEQ ID 7284; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 563 BP; 141 A; 140 C; 109 G; 158 T; 15 other:

Query Match 65.7%; Score 18.4; DB 22; Length 563;
Best Local Similarity 78.6%; Pred. No. 83;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Caps 0;

0Y 1 AAATTGGTACAAGATGATACCTTCGTT 28
1 ||||| ||| || ||||| ||
Db 356 ATATTGGAAACATGCTACCTTCCTT 329

```

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 ; Search time 607.084 Seconds

(Without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579A-18

Perfect score: 28
Sequence: 1 aaatgggtacacagatgatacctcgtt 28Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_Da:*
2: gb_Htg:*
3: gb_In:*
4: gb_Om:*
5: gb_Ov:*
6: gb_Pat:*
7: gb_Pb:*
8: gb_Pl:*
9: gb_Pr:*
10: gb_Ro:*
11: gb_Sts:*
12: gb_Sy:*
13: gb_Un:*
14: gb_Vi:*
15: em_Da:*
16: em_Fun:*
17: em_Hum:*
18: em_In:*
19: em_Mu:*
20: em_Om:*
21: em_Or:*
22: em_Ov:*
23: em_Pat:*
24: em_Ph:*
25: em_Pl:*
26: em_Ro:*
27: em_Sts:*
28: em_Un:*
29: em_Vi:*
30: em_Htg_Hum:*
31: em_Htg_Inv:*
32: em_Htg_Other:*
33: em_Htg_Mus:*
34: em_Htg_Pln:*
35: em_Htg_Rod:*
36: em_Htg_Man:*
37: em_Htg_Vit:*
38: em_Sy:*
39: em_Htgo_Hum:*
40: em_Htgo_Mus:*
41: em_Htgo_Other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	28	100.0	28	6	AX306859	AX306859 Sequence
2	28	100.0	1789	6	E09772	E09772 The base se
3	28	100.0	2007	6	AR089410	AR089410 Sequence
4	28	100.0	2007	6	AR093610	AR093610 Sequence
5	28	100.0	2322	1	SABBP	Y00688 Staphylococ
6	28	100.0	2322	6	E03736	E03736 DNA sequenc
7	28	100.0	2454	1	SEMECAPB	X52592 S. epidermi
8	28	100.0	2455	6	E09771	E09771 The base se
9	28	100.0	2456	1	SAMECAPB	X52593 S. aureus m
10	28	100.0	2456	6	AX110445	AX110445 Sequence
11	28	100.0	5596	1	SSK3MECA	Y13096 S.sciuri me
12	28	100.0	6368	1	SSK3MECA2	Y13095 S.sciuri me
13	28	100.0	9047	1	SAMECARL1	Y14051 Staphylococ
14	28	100.0	21777	1	AB063173	AB063173 Staphyloc
15	28	100.0	26090	1	AB063172	AB063172 Staphyloc
16	28	100.0	39332	1	AB033763	AB033763 Staphyloc
17	28	100.0	58237	1	D86934	D86934 Staphylococ
18	28	100.0	290250	1	AP004822	AP004822 Staphyloc
19	28	100.0	298050	1	AP003129	AP003129 Staphyloc
20	28	100.0	349999	1	AB003358	AB003358 Staphyloc
21	26.4	94.3	68256	1	AB037671	AB037671 Staphyloc
22	21.8	77.9	272258	2	AC123866	AC123866 Mus muscu
23	20.6	73.6	2012	10	HAM.LTR6BH	M73592 Mesocricetu
24	20.2	72.1	5068	1	SSK1MECA	Y09223 S.sciuri me
25	20.2	72.1	6684	1	SSK1MECA	Y13094 S.sciuri me
26	20	71.4	3800	6	AX416707	AX416707 Sequence
27	20	71.4	103705	2	AC110641	AC110641 Rattus no
28	20	71.4	161799	2	AC111516	AC111516 Rattus no
29	20	71.4	186728	2	AC111099	AC111099 Mus muscu
30	20	71.4	219471	2	AL772341	AL772341 Mus muscu
31	19.8	70.7	86487	9	AL592157	AL592157 Human DNA
32	19.8	70.7	174700	2	AC025344	AC025344 Homo sapi
33	19.6	70.0	194907	2	AC106835	AC106835 Mus muscu
34	19.6	70.0	198421	2	AC125180	AC125180 Mus muscu
35	19.2	68.6	112286	2	AP005556	AP005556 Oryza sat
36	19.2	68.6	117737	8	F6D8	AC008016 Arabidops
37	19.2	68.6	127824	9	AC004822	AC004822 Homo sapi
38	19.2	68.6	161955	9	AC068718	AC068718 Homo sapi
39	19.2	68.6	179993	9	AC018360	AC018360 Homo sapi
40	19	67.9	30626	3	CE16A11	Z81505 Caenorhabdi
41	19	67.9	45350	9	AC084398	AC084398 Homo sapi
42	19	67.9	60931	2	AC105113	AC105113 Homo sapi
43	19	67.9	66397	2	AC117548	AC117548 Mus muscu
44	19	67.9	111851	9	AC090564	AC090564 Homo sapi
45	19	67.9	125866	8	OSJN00283	AL731638 Oryza sat

ALIGNMENTS

RESULT 1
AX306859
LOCUS
DEFINITION
AX306859
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
SYNTHETIC CONSTRUCT.
synthetic construct
artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL
Taya, T., Ishiguro, T. and Saito, J.
Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
Patent: EP 1160333-A 18 05-DEC-2001;

Tosoh Corporation (JP)
Location/Qualifiers
1. 28
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 9 a 4 c 6 g 9 t

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATGATACCTTCGTT 28
|||||
1 AAATTGGGTACAGATGATGATACCTTCGTT 28

Db 1 AAATTGGGTACAGATGATGATACCTTCGTT 28

RESULT 2
E09772 1789 bp RNA linear PAT 29-SEP-1997
XCUS The base sequence of modified meca DNA.
DEFINITION E09772
ACCESSION E09772.1 GI:22026401
VERSION JP 1995209294-A/2.
KEYWORDS Staphylococcus aureus.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1 (bases 1 to 1789)
AUTHORS Kono, M., Hiramatsu, K., Sasazu, M., Noguchi, M. and Suguro, K.
TITLE NOVEL MECA PROMOTER, CODING DNA THEREFOR, AND DETECTION METHOD FOR METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL Patent: JP 1995209294-A 2, 11-AUG-1995;
COMMENT KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/2
PD 11-AUG-1995
PF 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI MASAHISA,
PI SUGURO KAZUYA
PC G01N33/53, C07K14/31, C12N1/21, C12M15/09, C12P21/02, (C12N1/21, PC C12N1.19);
PC (C12P21/02, C12N1.19);
CC strandedness: Double;
CC topology: Linear;
FH key Location/Qualifiers
FH source 1. 1789
FT /organism="Staphylococcus aureus" FT CDS
FT 1. 1608 /product="Modified meca".
FT Location/Qualifiers
FEATURES
source 1. 1789
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"
BASE COUNT 735 a 263 c 302 g 489 t

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 1789;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATGATACCTTCGTT 28
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1 AAATTGGGTACAGATGATGATACCTTCGTT 28

Db 203 AAATTGGGTACAGATGATGATACCTTCGTT 230

RESULT 3
AR089410 2007 bp DNA linear PAT 07-SEP-2000
LOCUS AR089410
DEFINITION Sequence 169 from patent US 5994066.
ACCESSION AR089410

VERSION AR089410.1 GI:10016167
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2007)
AUTHORS Bergeron, M.G., Picard, F.J., Ouellette, M. and Roy, P.H.
TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 5994066-A 169 30-NOV-1999;
FEATURES
source 1. 2007
Location/Qualifiers
BASE COUNT 855 a 270 c 341 g 541 t

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATGATACCTTCGTT 28
|||||
1 AAATTGGGTACAGATGATGATACCTTCGTT 28

Db 608 AAATTGGGTACAGATGATGATACCTTCGTT 635

RESULT 4
AR093610 2007 bp DNA linear PAT 08-SEP-2000
LOCUS AR093610
DEFINITION Sequence 169 from patent US 6001564.
ACCESSION AR093610
VERSION AR093610.1 GI:10020359
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2007)
AUTHORS Bergeron, M.G., Ouellette, M. and Roy, P.H.
TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 6001564-A 169 14-DEC-1999;
FEATURES
source 1. 2007
Location/Qualifiers
BASE COUNT 855 a 270 c 341 g 541 t

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATGATACCTTCGTT 28
|||||
1 AAATTGGGTACAGATGATGATACCTTCGTT 28

Db 608 AAATTGGGTACAGATGATGATACCTTCGTT 635

RESULT 5
SABP 2322 bp DNA linear BCT 12-SEP-1993
LOCUS SABP
DEFINITION Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible penicillin-binding protein.
ACCESSION Y00688
VERSION Y00688.1 GI:46628
KEYWORDS penicillin-binding protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1 (bases 1 to 2322)
AUTHORS Song, M.D., Machi, M., Doi, M., Ishino, F. and Matsushashi, M.
TITLE Evolution of an inducible penicillin-target protein in

methicillin-resistant *Staphylococcus aureus* by gene fusion
 JOURNAL EMBL Lett. 221 (1), 167-171 (1987)
 MEDLINE 87304805
 PUBMED 3305073
 REFERENCE 2 (bases 1 to 2322)
 AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
 Barberis-Maino, L., Kayser, F. H. and Berger-Bachli, B.
 Title Sequence comparison of meca genes isolated from
 methicillin-resistant *Staphylococcus aureus* and *Staphylococcus*
epidermidis
 JOURNAL Gene 94 (1), 137-138 (1990)
 MEDLINE 91033056
 PUBMED 2227446
 COMMENT Data kindly reviewed (13.1.88) by Matsubashi.
 FEATURES
 source Location/Qualifiers
 1..2322
 /organism="Staphylococcus aureus"
 /db_xref="taxon:1280"
 1..2013
 /note="penicillin-binding protein (AA 1-670)"
 /codon_start=1
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 /db_xref="GI:46629"
 /db_xref="SWISS-PROT:P07944"
 /translation="MKIKIVPLILVVVGFQIYFASKDKELNNTDAIEDKNEKQ
 VYKDSYISKSDNGEVEEMTERPIKIYNSLQKINIDARKIKYKSKKKRYDAQYKIK
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 ELANTGTNMLRGIVPKVSKKQYKAIKESTSEDYNNKMKIIGYKMFSEFKTVK
 KMDYSDPFAKKFHLTNTFESNRNPLGCVYVGNINSEELKOKRYKQKDDA
 VIGKKLEKLYDKKLOHEDYRPTIYAVDNCVIAHTLEKKKROKROQUTIDAV
 OKSTLYNMKNDYSGTAIHQTEGLALVSTPSDYVPFWYGSNEYNLTEDEKRP
 LNKFOITTPSPGQKILTFAMIGLNNNTLDDKSYKIDGQWQKDSWGWYNTREY
 VNGNIDKQAIIESDNIFPAVALELGSKFEKMGKLGVEDIPSPYPPYNAQISNK
 NLDEILLDSDGGEILINPOILISYALENGNINPHILKDTKNNKMKNIIS
 KENINILNDGMOGVNKTKEIDYRSYANLIGSGTLELKMKGCEGTQKQWFISSYDK
 DNPMMMAINVKDQDKMASYNAKISGVYDELYENGNNKKYDIDE"
 BASE COUNT 940 a 324 c 389 g 669 t
 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAATTGGTACAGATGATACCTTCGTT 28
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 Db 608 AAATTGGTACAGATGATACCTTCGTT 635
 RESULT 6
 LOCUS E03736 2322 bp DNA linear PAT 29-SEP-1997
 DEFINITION DNA sequence of PBP2' gene for determination of methicillin
 resistance.
 VERSION E03736.1 GI:2171951
 KEYWORDS JP 1992169200-A/9.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 2322)
 AUTHORS Watanabe, Y., Nakamura, E., Teraoka, H., Wada, K., Minamide, W. and
 Murakami, K.
 TITLE DETECTION OF PBP 2' GENE AND JUDGEMENT OF METHICILLIN RESISTANCE
 JOURNAL Patent: JP 1992169200-A 9 17-JUN-1992;
 SHIONOGI & CO LTD
 OS (methicillin resistant)staphylococcus aureus
 PN JP 1992169200-A/9
 PD 17-JUN-1992
 PF 31-OCT-1990 JP 1990296708
 PI WATANABE YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI,
 MI NAMIDE WAKIO, MURAKAMI KAZUHIISA
 PC C1201/68,C12N15/11;

CC strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH Key Location/Qualifiers
 FT misc_feature 1..2322
 /note="'PBP2' gene for determination of
 methicillin
 resistance'
 FT Location/Qualifiers
 1..2322
 /organism="unidentified"
 /db_xref="taxon:32644"
 BASE COUNT 939 a 324 c 390 g 669 t
 ORIGIN
 Query Match 100.0%; Score 28; DB 6; Length 2322;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AAATTGGTACAGATGATACCTTCGTT 28
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 Db 608 AAATTGGTACAGATGATACCTTCGTT 635
 RESULT 7
 LOCUS SEMECAPB 2454 bp DNA linear BCT 12-SEP-1993
 DEFINITION S. epidermidis meca gene for PBP2' (penicillin binding protein 2').
 ACCESSION X52592.1 GI:46993
 VERSION X52592
 KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
 penicillin-binding protein 2;
 Staphylococcus epidermidis.
 SOURCE Staphylococcus epidermidis
 ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
 REFERENCE 1 (bases 1 to 2448)
 AUTHORS Ryffel, C.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
 Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
 REFERENCE 2 (bases 1 to 2454)
 AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
 Barberis-Maino, L., Kayser, F. H. and Berger-Bachli, B.
 TITLE Sequence comparison of meca genes from methicillin-resistant
 Staphylococcus aureus and Staphylococcus epidermidis
 JOURNAL Gene (1990) In press
 REFERENCE 3 (bases 1 to 2454)
 AUTHORS Ryffel, C.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUL-1990) Ryffel C., University of Zuerich, Inst of
 Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
 REFERENCE 4 (bases 1 to 2454)
 AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
 Barberis-Maino, L., Kayser, F. H. and Berger-Bachli, B.
 TITLE Sequence comparison of meca genes isolated from
 methicillin-resistant *Staphylococcus aureus* and *Staphylococcus*
epidermidis
 JOURNAL Gene 94 (1), 137-138 (1990)
 MEDLINE 91033056
 PUBMED 2227446
 COMMENT See also <X52593-4> and <X00688>.
 Data kindly reviewed (23-JUL-1990) by C. Ryffel.
 FEATURES
 source Location/Qualifiers
 1..2454
 /organism="Staphylococcus epidermidis"
 /strain="WT55"
 /db_xref="taxon:1282"
 /clone="WT80/WT79"
 80..85
 /note="35 region"
 101..105
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RBS /note=-10 region"
130..134
/note="ribosome binding site"
precursor_RNA 141..2159
/note="primary transcript"
141..2147
/note="PBP2' (AA 1 - 668)"
/codon_start=1
/transl_table=1
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/db_xref="GI:46994"
/db_xref="SPTREMBL:054113"
/translation="MKKIKIVPLILIVVVGVIYFVASKKEINNTIDATEDKNEKO
VKKDSYTSKSDNCEVEETERP IRTYNSLGKODINIDQR IKKVSKNKKRPDAQTKIK
TNGNIDNRKVOFNFVKEDGMK LMDHSHV IIPGMDKDS IHIENLSERGKILDRNNV
ELANTGVAIEIGIVPRNVSKDKYKAIAELIS ESDY I KOOMQDNVODDTVEPIKTVK
KMDYLSDFAPAK FHLTJNTEESRNPPLGKAVSHLIGYGP IINSEELKOEKGYKDA
VYKKGLEKLYDKLQIHEDGYRVTIVDONSNT IAHTLLEKKKDKGDIOLTDIAVOK
SIYNNKNDVGSSTGAIHPOTGELLALVSTPSYDVPFMYGMSNEEYNKLTEDKKEPIL
NKFOITSPGSTOKITITAMIGLINNKTLLDDKTSYKIDGKMDKSKWGVNTRYEVN
CNIDLKQIESDNIFFARVALELCSKFEKOMKLGVEDIPSDPYPRYNAQISKNL
DNEILLADSGYGGCEILINPVQILSIYSALENGNINAPHLIKTRKNVYMKNIISKE
NINLITDMQOVNKTTHKEDIYRSYANLIGSGTAELEMKOGETGROIQWFIISYDKDN
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old_sequence 441..448
/note="altaaac was ac in [1]"
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old_sequence 641..643
/note="agc was ac in [1]"
/citation=[1]
old_sequence 652..653
/note="ta was tta in [1]"
/citation=[1]
old_sequence 731..733
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old_sequence 780..781
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BASE COUNT 997 a 345 c 398 g 714 t
ORIGIN
Query Match 100.0%; Score 28; DB 1; Length 2454;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 A A A T T G G T A C A A G A T G A T A C C T T C G T T 28
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749 A A A T T G G T A C A A G A T G A T A C C T T C G T T 776
|||||
RESULT 8
LOCUS E09771 2455 bp RNA linear PAT 29-SEP-1997
DEFINITION The base sequence of meca DNA.
ACCESSION E09771
VERSION E09771.1 GI:22026400
KEYWORDS JP 1995209294-A/1.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
1 (bases 1 to 2455)
REFERENCE Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
AUTHORS NOVEL 'MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
TITLE METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL PATENT: JP 1995209294-A 1 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/1
PD 11-AUG-1995
PF 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
MASAHISA,

PI SUGURO KAZUHA
PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,(C12N1/21, PC
C12R1:19),
PC (C12P21/02,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1..2455
FT 134..2146 /organism='Staphylococcus aureus' FTY CDS
FT 134..2146 /product='meca protein'.
FEATURES
source Location/Qualifiers
1..2455
/organism='Staphylococcus aureus'
/db_xref="taxon:1280"
BASE COUNT 997 a 344 c 401 g 713 t
ORIGIN
Query Match 100.0%; Score 28; DB 6; Length 2455;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 A A A T T G G T A C A A G A T G A T A C C T T C G T T 28
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741 A A A T T G G T A C A A G A T G A T A C C T T C G T T 768
|||||
RESULT 9
SAMECAPB 2456 bp DNA linear BCT 12-SEP-1993
LOCUS S. aureus meca gene for PBP2' (penicillin binding protein 2).
DEFINITION X52593
ACCESSION X52593
VERSION X52593.1 GI:46610
KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
pen.,illin-binding protein 2.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
1 (bases 1 to 2456)
REFERENCE Ryffel,C.
AUTHORS Direct Submission
TITLE Submitted (05-Apr-1990) Ryffel C., University of Zuerich, Inst of
JOURNAL Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
2 (bases 1 to 2456)
REFERENCE Ryffel,C., Tesch,M., Birch-Machin,I., Reynolds,P.E.,
AUTHORS Harberis-Maino,L., Kayser,F.H. and Berger-Bachi,B.
TITLE Sequence comparison of meca genes isolated from
methicillin-resistant Staphylococcus aureus and Staphylococcus
epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT See also <X52592> and <X00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.
FEATURES
source Location/Qualifiers
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/db_xref="taxon:1280"
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/promoter /note="-35 region"
101..105
/promoter /note="-10 region"
130..134
RBS /note="ribosome binding site"
141..2153
precursor_RNA /note="primary transcript"
141..2147
CDS /note="PBP2' (AA 1-668)"
/codon_start=1
/transl_table=1

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ELANTGTHMRGLIVPKNVSKDKYAIKAEKISISDYYINNMKIGYMIISPHKTYK
KMDYELSDPAKKRHLTTNTERESRNYPLEKATSHLGYCPINSEELKOKEKYKQKDA
VIOKRGLEKLDKLOHEDGRTYIVDNSNTIAHTLIEKKRKGKIDLTIDAKYVK
STYNNMNDVSGSGAIHPQTEGELALVSTSYDYPWPYGMSNEEYKLTEDKREPL
NKFOITTSPTSGTILTPAMIGLNKKTLDDSTYKIDGMOQKDSMGVYVTRREVN
GNIDKQAISSDNIFFARVALIEGSKPEKGMKLCQVEDIPSDYPPYAOISNKL
DNELLADSGYGOEILINPVOLISYSALENNONINAPHLKIDTKKWKKNIKISKE
NINLIMQGVVKKTHKEDIYRSYANLICKSGYAEILKMKOGESGRQIGMFIYSKDN
PNMMAINVDVODKMASTRNAKISGVYDELYENGNKKYDIDE"

BASE COUNT 1001 a 344 c 396 g 715 t
ORIGIN

Query Match 100.0%; Score 28; DB 1; Length 2456;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATTGGGTACAGATGATACCTTCGTT 28
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Db 748 AATTGGGTACAGATGATACCTTCGTT 775

RESULT 10
AX110445
LOCUS AX110145 2456 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 1178 from Patent WO0123604.
ACCESSION AX110445
VERSION AX110445.1 GI:13926737
KEYWORDS
SOURCE
ORANISM Staphylococcus aureus subsp. aureus NCTC 8325.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
AUTHORS 1 (bases 1 to 2456)
Bergeon, M.G., Bolesinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
Picard, F.J. and Roy, P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1178 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
Source 1. 2456
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/db_xref="taxon:33061"
ASE COUNT 1001 a 344 c 396 g 715 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2456;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATTGGGTACAGATGATACCTTCGTT 28
|||||
Db 748 AATTGGGTACAGATGATACCTTCGTT 775

RESULT 11
SSK8MECA
LOCUS SSK8MECA 5596 bp DNA linear BCT 16-JAN-1998
DEFINITION S.sciuri meca gene, strain K8 (ATCC700063).
ACCESSION Y13096
VERSION Y13096.1 GI:2791919
KEYWORDS meca gene; mecI gene; mTORF78; mTORF78; ORF142.
SOURCE Staphylococcus sciuri.
ORANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 5596)
AUTHORS Wu, S., de Lencastre, H. and Tomasz, A.
TITLE Genetic organization of the meca region in methicillin-susceptible

and methicillin-resistant strains of Staphylococcus sciuri
J. Bacteriol. 180 (2), 236-242 (1998)

JOURNAL
MEDLINE 98101461
PUBMED 9440511
REFERENCE 2 (bases 1 to 5596)
AUTHORS Wu, S.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences X53818, X54660, L14020, X52593, Y09223.
FEATURES
source
1. 5596
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/strain="K8 (ATCC700063)"
/sub_species="rodentius"
/db_xref="taxon:1296"
1. 236
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1. 236
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/db_xref="SPTREMBL:054284"
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GIEICVALYKKNRRSLQYGFSPCHSISIMLAS"
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/codon_start=1
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/translation="MDNKTYEISSAEWEVWNIIMKKYASANYIEIIOKOKNSPKT
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/protein_id="CAA73546.1"
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HITISYSSNINPNVYFGLKSOIYVTVETIMDKREIYILIELSHVSKHDIFFNO
LHYVFKMIFMFPALYISKTMMNDNCEVCDRNVLILNHEHRIYCESILKCSILKS
OHNNVNAOYLLGFNSNIKERKVIYALDSMPKPNRKRIVAYIVCSISILLIOAPLS
AHVOODKRETVSYKKLNLOLAPFKGFCGSPVLNNEBOAIVSNIPESQORSYDPSNT
KYIYALMAEPQNLISLNHTEQMDKQHPFKENQDONLSSSKYSVNYTYENTLNKH
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complement(2638..2643)
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complement(2663..2668)

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RBS            2702. .2707
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                  2713. .4719
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                  /db_xref="GI:2791923"
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VVKDSSYISKSDNGEVEWTERPIKLYNSLGVADINTODRKIKVSKNKRKRVDAQYKIK
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ELANTGTAVEIGIVPKNSKDKYKAKALAKELTISEDYIKQOQDQNMVQDDPEVPLTVK
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STYNNKNDGSGTAIHPOGELIALVSTPSTDVTPFMTGMSNEEYNNKLTEDKKEPL
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GNIDLKQALIESSDNIPFARVALELQSKRFEKMGKLGVEDIPSDYPPYNAQISNNL
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gene            complement(4765. .5266)
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gene            /gene="ORF142"
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CDS            /gene="NTORF101"
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BASE COUNT     1991 a      856 c      821 g     1928 t
ORIGIN
Query Match     100.0%; Score 28; DB 1; Length 5596;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AAATGGCTACAAGATCATCTCGTT 28
Db      3321 AAATGGGTACAGATGATACCTTCGTT 3348
RESULT 12
SSK3MECA2
LOCUS      SSK3MECA2      6368 bp      DNA      linear      BCT 16-JAN-1998
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DEFINITION      S. sciuri meca2 gene, strain K3 (MM2).
ACCESSION       Y13095
VERSION         Y13095.1 GI:2791912
KEYWORDS        CTORF261 gene; meca2 gene; mecI gene; mecR1 gene; NTORF101; ORF142.
SOURCE          Staphylococcus sciuri.
ORGANISM        Staphylococcus sciuri
REFERENCE       1 (bases 1 to 6368)
AUTHORS         Wu,S., de Lencastre,H. and Tomasz,A.
TITLE           Genetic organization of the meca region in methicillin-susceptible
                and methicillin-resistant strains of Staphylococcus sciuri
JOURNAL         J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE        98101461
PUBMED         9440511
REFERENCE       2 (bases 1 to 6368)
AUTHORS         Wu,S.
TITLE           Direct Submission
JOURNAL         Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
                University, 1230 York Avenue, New York NY 10021, USA
                Related sequences L14020, X52593, Y09223.
FEATURES        Location/Qualifiers
                 1..6368
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BASE COUNT	2230 a 996 c 884 g 2256 t	
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Query Match	100.0%; Score 28; DB 1;	Length 6368;
Best Local Similarity	100.0%; Pred. No. 0.011;	
Matches 28:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 AAATTGGTACAGATGATACCTTCGT 28 AAAAAAAAAAAAAAAAAAAAA	
Db	4093 AAAATTGCCTACAGATGATACCTTCGTT 4120	
RESULT 13		
SAMECARL1	9047 bp	DNA linear BCT 16-JAN-1998
LOCUS		
DEFINITION	Staphylococcus aureus mecM, mecR1 gene and ORF142, ORF142, ORF44, ORF145 and ORF224.	
ACCESSION	V14051	
VERSION	V14051.1 GI:2791983	
KEYWORDS	mecM gene; mecI gene; mecR1 gene; ORF142; ORF145; ORF224; ORF44; PBP2A; repressor protein; transposase.	
SOURCE	Staphylococcus aureus	
ORGANISM	Bacteria; Firmicutes; Bacillales; Staphylococcus.	
REFERENCE	1 (bases 1 to 9047)	
AUTHORS	Wu,S.	
TITLE	Direct Submission	
JOURNAL	Submitted (27-JUN-1997) S. Wu, Laboratory of Microbiology, The Rockefeller University, 1230 York Avenue, New York, NY 10021, USA	
REFERENCE	2 (bases 1 to 9047)	
AUTHORS	Wu,S., de Lencastre,H. and Tomasz,A.	
TITLE	Genetic organization of the mecA region in methicillin-susceptible and methicillin-resistant strains of Staphylococcus sciuri	
JOURNAL	J. Bacteriol. 180 (2), 236-242 (1998)	
MEDLINE	98101461	
PUBMED	9440511	
FEATURES		
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gene		

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        HITISYSSNIDNPMVFLVKSQIVLPVTVEVTEINDEETITLHELSHVSQHLIFNO
        LYVFMKTFENFALTSKTMNDNDEKCDRVNLILNHEHIRGESLTKSLKLS
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        AHVQODKRETVNSYKKNLQALPYKGFDSFVLYNERQAYSIYNESPESKQYSPST
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        VIOKCLELIDKRIKQHEPGYRVTVIDVDSNTIAHLIEKKKMDGKDIDLTTDAKQK
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BASE COUNT      3099 a 1469 c 1257 g 3222 t
ORIGIN
Query Match      100.0%; Score 28; DH 1; Length 9047;
Best Local Similarity 100.0%; Pred No. 0.01;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY      1 AAATTGGGTACAGATGATGATCCTTCGTT 28
Db      4079 AAATTGGGTACAGATGATGATCCTTCGTT 4106
RESULT 14
AB063173      21777 bp      DNA      linear      BCT 09-APR-2002
LOCUS      Staphylococcus aureus DNA, type-IV staphylococcal cassette
DEFINITION      chromosome mec, strain:JCS1978(8/6-3p).
ACCESSION      AB063173
VERSION      AB063173.1 GI:17025993
KEYWORDS      Staphylococcus aureus (strain:JCS1978(8/6-3p)) DNA.
SOURCE      Staphylococcus aureus
ORGANISM      Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE      1 Hiramatsu,K., Cui,L., Kuroda,M. and Ito,T.
AUTHORS      The emergence and evolution of methicillin-resistant Staphylococcus
TITLE      aureus Microbiol. 9 (10), 486-493 (2001)
JOURNAL      Trends Microbiol. 9 (10), 486-493 (2001)
MEDLINE      21482917
AUTHORS      Ma,X.X., Ito,T., Tienasastorn,C., Jamklang,M., Chongtrakool,P.,
TITLE      Boyle-Vavra,S., Damm,R.S. and Hiramatsu,K.
JOURNAL      Novel type of Staphylococcal Cassette Chromosome mec identified in
TITLE      Community-Acquired Methicillin-Resistant Staphylococcus aureus
JOURNAL      Strains
JOURNAL      Antimicrob. Agents Chemother. 46 (4), 1147-1152 (2002)
MEDLINE      21895198
AUTHORS      3 (bases 1 to 21777)
REFERENCE      Xue,M.X., Ito,T., Hiramatsu,K. and Tienasastorn,C.
AUTHORS      Direct Submission
JOURNAL      Submitted (12-JUN-2001) Terryu Ito, Juntendo University, Department
TITLE      of Bacteriology, Hongo 2-1-1, Bunkyo-Ku, Tokyo 113-8421, Japan
TITLE      (E-mail:teruyabac@med.juntendo.ac.jp, Tel:81-3-5802-1041,
TITLE      Fax:81-3-5684-7830)
FEATURES
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SRKSIIVLMYGPSCVGTKEMLIISECIGKLPKROMSKNTKMPDIIFNNHGPS
LARDLLRESNIVLLDFPDKGVNELNSAFYOLPDEGIJEDSOYKVTMNSIILICTSNP
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RESULT 15
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DEFINITION      Staphylococcus aureus DNA, type-IV staphylococcal cassette
KEYWORDS      Staphylococcus aureus
SOURCE      Staphylococcus aureus (strain:JCSC 1968 (CA05)) DNA.
ORGANISM      Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE      1
AUTHORS      Hiramatsu, K., Cui, L., Kuroda, M. and Ito, T.
TITLE      The emergence and evolution of methicillin-resistant Staphylococcus
JOURNAL      Trends Microbiol. 9 (10), 486-493 (2001)
MEDLINE      21482917
REFERENCE      2
AUTHORS      Ma, X. X., Ito, T., Tienasastorn, C., Jamklang, M., Chongtrakool, P.,
            Boyle-Vavra, S., Daum, R. S. and Hiramatsu, K.
TITLE      Novel Type of Staphylococcal Cassette Chromosome mec Identified in
            Community-Acquired Methicillin-Resistant Staphylococcus aureus
            Strains
JOURNAL      Antimicrob. Agents Chemother. 46 (4), 1147-1152 (2002)
MEDLINE      21895198
REFERENCE      3 (bases 1 to 26090)
AUTHORS      Xue, M. X., Ito, T., Hiramatsu, K. and Tienasastorn, C.
TITLE      Direct Submission
JOURNAL      Submitted (12-JUN-2001) Tetsuyo Ito, Juntendo University, Department
            of Bacteriology, Hongo 2-1-1, Bunkyo-ku, Tokyo 113-8421, Japan
            (E-mail: tetsuyabacmed.juntendo.ac.jp, Tel: 81-3-5802-1041,
            Fax: 81-3-5684-7830)
COMMENT      On Mar 11, 2002 this sequence version replaced gi:17025971.
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATTGGTACAGATGATACCTTCGTT 28
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DB 18254 AAATTGGTACAGATGATACCTTCGTT 18281

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Job time : 619.209 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 ; Search time 433.631 Seconds

(without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579A-21

Perfect score: 20

Sequence: 1 gtagtggaatattgtgcc 20

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	20	6	AX306862	AX306862 Sequence
3	20	100.0	39	6	AX306869	AX306869 Sequence
4	20	100.0	1789	6	E09772	E09772 The base se
5	20	100.0	2007	6	AR089410	AR089410 Sequence
6	20	100.0	2007	6	AR093610	AR093610 Sequence
7	20	100.0	2322	6	SABP	Y00688 Staphylococ
8	20	100.0	2322	6	E03736	E03736 DNA sequenc
9	20	100.0	2454	6	SEMECAPB	X52592 S. epidermi
10	20	100.0	2455	6	SEMECAPB	E09771 The base se
11	20	100.0	2456	6	AX110445	X52593 S. aureus m
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14	20	100.0	6368	1	SSK3MECA2	Y13095 S. sciuri me
15	20	100.0	9047	1	SSK3MECA1	Y14051 Staphylococ
16	20	100.0	21777	1	AB063173	AB063173 Staphyloc
17	20	100.0	26090	1	AB063172	AB063172 Staphyloc
18	20	100.0	39332	1	AB033763	AB033763 Staphyloc
19	20	100.0	58237	1	D86934	D86934 Staphylococ
20	20	100.0	68256	1	AB037671	AB037671 Staphyloc
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ALIGNMENTS

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DEFINITION Sequence 11 from Patent EP1160333.
ACCESSION AX306852
VERSION AX306852.1 GI:17894674
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 Taya, T., Ishiguro, T. and Saito, J.
Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
Patent: EP 1160333-A 11 05-DEC-2001;
JOURNAL
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FEATURES Tosoh Corporation (JP)
Source Location/Qualifiers
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BASE COUNT 4 a 3 c 4 g 9 t

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Db 1 GTTAGTGAATATCTTGCC 20

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DEFINITION Sequence 21 from Patent EP1160333.
ACCESSION AX306862
VERSION AX306862.1 GI:17894684
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.

REFERENCE 1
AUTHORS Taya,T., Ishiguro,T. and Saito,J.
TITLE Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
Patent: EP 1160333-A 21 05-DEC-2001;
JOURNAL
Tosoh Corporation (JP)
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BASE COUNT 4 a 3 c 4 g 9 t

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1 GTTAGTGAATATCTTGCC 20

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LOCUS AX306869 39 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 28 from Patent EP1160333.
ACCESSION AX306869
VERSION AX306869.1 GI:17894691
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.

REFERENCE 1
AUTHORS Taya,T., Ishiguro,T. and Saito,J.
TITLE Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
Patent: EP 1160333-A 28 05-DEC-2001;
JOURNAL
Tosoh Corporation (JP)
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Db 1 GTTAGTGAATATCTTGCC 20

RESULT 4
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LOCUS E09772 1789 bp RNA linear PAT 29-SEP-1997
DEFINITION The base sequence of modified meca DNA.
ACCESSION E09772
VERSION E09772.1 GI:22026401
KEYWORDS
SOURCE
ORGANISM
Staphylococcus aureus.
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1
AUTHORS Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
TITLE NOVEL 'MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
Patent: JP 1995209294-A 2 11-AUG-1995;
JOURNAL
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/2
PD 11-AUG-1995
PF 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
MASAHISA
PI SUGURO KAZUYA
PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC
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DEFINITION Sequence 169 from patent US 5994066.
ACCESSION AR089410
VERSION AR089410.1 GI:10016167
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2007)

AUTHORS Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.
 TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
 JOURNAL Patent: US 5994066-A 169 30-NOV-1999;
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 DEFINITION Sequence 169 from patent US 6001564.
 ACCESSION AR093610
 VERSION AR093610.1 GI:10020359
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 2007)
 AUTHORS Bergeron,M.G., Ouellette,M. and Roy,P.H.
 TITLE Species specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
 JOURNAL Patent: US 6001564-A 169 14-DEC-1999;
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GTTACTGTAATATCTTTGCC 20
 Db 980 GTTACTGTAATATCTTTGCC 961

RESULT 7
 SABP/c 2322 bp DNA linear BCT 12-SEP-1993
 LOCUS staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible penicillin-binding protein.
 ACCESSION Y00688
 VERSION Y00688.1 GI:46628
 KEYWORDS penicillin-binding protein.
 SOURCE Staphylococcus aureus.
 ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
 REFERENCE 1 (bases 1 to 2322)
 AUTHORS Song,M.D., Wachi,M., Doi,M., Ishino,F. and Matsushashi,M.
 TITLE Evolution of an inducible penicillin-target protein in methicillin-resistant Staphylococcus aureus by gene fusion
 JOURNAL FEBS Lett. 221 (1), 167-171 (1987)
 MEDLINE 87304805
 PUBMED 3305073
 REFERENCE 2 (bases 1 to 2322)
 AUTHORS Kyifel,C., Teschn,W., Birch-Machin,I., Reynolds,P.E.,

TITLE Barberis-Maino,L., Kayser,F.H. and Berger-Bachi,H.
 Sequence comparison of mecA genes isolated from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis
 JOURNAL Gene 94 (1), 137-138 (1990)
 MEDLINE 91033056
 PUBMED 2227446
 COMMENT Data kindly reviewed (13.1.88) by Matsushashi.
 FEATURES Location/Qualifiers
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 /note="penicillin-binding protein (PA 1-670)"
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 /db_xref="GI:46629"
 /db_xref="SWISS-PROT:P07944"
 /translation="MKKIKIVPLILVVVVGCIYFYASKDKENNTIDAIEDKPKQ
 VYKDSYISKSDNGEVEETERPRIKIVNSLGVKDINIDRRIRKVSNNKRVDAQYKIK
 TVYGNIDRVVQNFVEKEDGMMKIDMDHSYIIPQMDQDSIIHLENLKSERKILDRNV
 ELANTGTHMRIGIVPRNVSCKDKAKAIKELISSEDIYNNKMKIRIGYKMIIPSEFKTVK
 KMDVYLDFAKKFHLTNETESRNPILGKATSHLIGYVPINSEFLKOKEYGYKQDA
 VIGKGLLEKLYDKLQIEDCYRYTVRVNDNSWTIAHTLIIEKKKIKGKDIQLTIDAKY
 OKSIYNNKNDYGSCTAIHPOTCELLAIYSTSYDYPTIGSNPEYKLTEDKREP
 LNKFEITTSFGSTOKILTAMIGLNKTLDDKTSYIDKGMQKQKSWGYNVTRREV
 VNGNIDLKQAISSDNIFFARVALDELSKRFEGMKLGVGEDIPSDYFVNAQISNK
 NLDENLIDSGYGOGEILINPQILSIYSALENNINAPILLIDTKRKVVKKNIS
 KENINLINDGMQOVNKTTHKEDIYRSYANILKSCFPAELKMKQCEGRQIGWYISYDK
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BASE COUNT 940 a 324 c 389 g 669 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTACTGTAATATCTTTGCC 20
 Db 986 GTTACTGTAATATCTTTGCC 967

RESULT 8
 LOCUS E03736 2322 bp DNA linear PAT 29-SEP-1997
 DEFINITION DNA sequence of PBP2' gene for determination of methicillin resistance.
 ACCESSION E03736
 VERSION E03736.1 GI:2171951
 KEYWORDS JP 1992169200-A/9.
 SOURCE unidentified.
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 2322)
 AUTHORS Watanabe,Y., Nakamura,E., Teraoka,H., Wada,K., Minamide,W. and Murakami,K.
 TITLE DETECTION OF PBP 2' GENE AND JUDGEMENT OF METHICILLIN RESISTANCE
 JOURNAL SHIONOGI & CO LTD
 OS (methicillin resistant)staphylococcus aureus
 PN JP 1992169200-A/9
 PD 17-JUN-1992
 PF 31-OCT-1990 JP 1990296708
 PI WATANABE YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI,
 PI MINAMIDE MAKIO, MURAKAMI KAZUHISA
 PC C1201/68, C12M15/11;
 CC strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH key location/Qualifiers

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FT      FT          /note="PBP2' gene for determination of FT
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Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTACTTGAAATATCTTTGCC 20
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Db 986 GTTACTTGAAATATCTTTGCC 967

/SUBT 9
/MECAPB/C
LOCUS      SEMECAPB 2454 bp DNA linear BCT 12-SEP-1993
DEFINITION S. epidermidis meca gene for PBP2' (penicillin binding protein 2').
ACCESSION X52592
VERSION X52592.1 GI:46993
KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
          penicillin-binding protein 2'.
SOURCE      Staphylococcus epidermidis.
            Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 2448)
AUTHORS Ryffel,C.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zurich, Inst of
REFERENCE Medical Microbiology, Gloriastr 32, CH-8028 Zurich, Switzerland
AUTHORS 2 (bases 1 to 2454)
          Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,
          Barberis-Maino,L., Kayser,F.H. and Berger-Baechi,B.
          Sequence comparison of meca genes from methicillin-resistant
          Staphylococcus aureus and Staphylococcus epidermidis
          Gene (1990) In press
          3 (bases 1 to 2454)
          Ryffel,C.
          Direct Submission
          Submitted (23-JUL-1990) Ryffel C., University of Zurich, Inst of
          Medical Microbiology, Gloriastr 32, CH-8028 Zurich, Switzerland
          4 (bases 1 to 2454)
          Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,
          Barberis-Maino,L., Kayser,F.H. and Berger-Baechi,B.
          Sequence comparison of meca genes isolated from
          methicillin-resistant Staphylococcus aureus and Staphylococcus
          epidermidis
          Gene 94 (1), 137-138 (1990)
JOURNAL MEDLINE
PUBMED 91033056
COMMENT See also <X52593-4> and <Y00688>.
          Data kindly reviewed (23-JUL-1990) by C. Ryffel.
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          /clone="WT80/WT79"
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          /note="primary transcript"
          141..2147
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ELANTGAYVEIGIYPRKNSKKDYKIAKELISEDY1KQMDQMWVODPTVPIKTVK
KMEVLSDFPAKFILTTNETESRNPPLGKATSHLIGVGPINSREIKOKERYKGVDA
VIGKGLKEKLYDKLOHEDGVRVTVDDNSNTIAHTLEKKKDGKDIOLIDAKVOK
SYNNKNDYSGSTRAIHPOGELLALVSTPGVDYPFMYGMSNEEYNTLTDDKPEPL
MKFOITTSFGSKITLTMIGLNNKTITLDDKTSYKIDGKMGKDKSMGCTNTRREYVH
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old_sequence 731..733
/note="caa was ca in [1]"
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/note="ct was ctt in [1]"
/citation=[1]
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Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTACTTGAAATATCTTTGCC 20
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Db 1120 GTTACTTGAAATATCTTTGCC 1101

RESULT 10
LOCUS      E09771/c 2455 bp RNA linear PAT 29-SEP-1997
DEFINITION The base sequence of meca DNA.
ACCESSION E09771
VERSION E09771.1 GI:22026400
KEYWORDS JP 1995209294-A/1.
SOURCE      Staphylococcus aureus.
ORGANISM    Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 2455)
AUTHORS Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
TITLE NOVEL 'MECA PROTEIN', CODING DNA THEREFOR, AND DETECTION METHOD FOR
JOURNAL METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
PUBMED Patent: JP 1995209294-A 11-AUG-1995;
COMMENT KONO MEGUMI, MITSUBISHI CHEM CORP., DENKA SEIKEN CO LTD
          Staphylococcus aureus
          PN JP 1995209294-A/1
          PD 11-AUG-1995
          PF 10-JAN-1994 JP 1994012226
          PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
          MASAHISA,
          PI SUGURO KAZUYA
          PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21,PC
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          PC (C12P21/02,C12N1.19);
          CC strandedness: Double;
          CC topology: Linear;

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134..2146 /product='meca protein'.
1..2455 location/Qualifiers
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Query Match 100.0%; Score 20; DB 6; Length 2455;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGTGAATATCTTGGC 20
1119 GTTAGTGAATATCTTGGC 1100
b 1119 GTTAGTGAATATCTTGGC 1100
RESULT 11
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LOCUS S. aureus meca gene for PBP2' (penicillin binding protein 2').
DEFINITION X52593.1 GI:46610
ACCESSION X52593.1 GI:46610
VERSION X52593.1 GI:46610
KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
penicillin-binding protein 2.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus
REFERENCE 1 (bases 1 to 2456)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS Ryffel, C.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zurich, Inst of
Medical Microbiology, Gloriastr 32, CH-8028 Zurich, Switzerland
REFERENCE 2 (bases 1 to 2456)
Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
Barberis-Maino, L., Kayser, F. H. and Berger-Bachli, B.
Sequence comparison of meca genes isolated from
methicillin-resistant staphylococcus aureus and staphylococcus
epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT See also <X52592>, <X52594> and <Y00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.
FEATURES
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101..105
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130..134
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141..2153
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141..2147
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ELANTGTHMFLGIVPRKNSKKDYAKAKELSISFDYINNNKIKIGYKMFSPFKTYK
KDEYLSDFAKKHEHTNETESRNPLEKATSHLGIVGPTINSELKQKKGKDDA
VICKGLEKLYDKKLOHEDGYRVT1VDDNSNT1AHTL1EKKKKNGK1Q1.T1DAKKVOK
SIYNNMNDYGSCTAIHPOTGELLALSTPSYDYVPRYGMSENEYKRLIEDKKEPLI
NKFOITTSPCSTOK11JAMIGLNKKTIDDKTSYK1DCKGQOKDSMGCVNTRYEVAN
GNIDLKQATSSSDNIFPARVALEIGSKKFEKGMKLGVDIPSDYFEYNAOISNNKL
DNEILLADSGGSEILLINPYOITISYSALENKNNTNAPILLKDTKKRYKKN1ISKE
NINLNDGMQDVNKTKEDEYRSYANLIGSGTAEKMKQGESGROIGMTSYDKDN
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BASE COUNT 1001 a 344 c 396 g 715 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 2456;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTA:TTGCAATATCTTGGC 20
1120 GTTAGTGAATATCTTGGC 1101
Db 1120 GTTAGTGAATATCTTGGC 1101
RESULT 12
AX110445/c 2456 bp DNA linear PAT 30-APR-2001
LOCUS AX110445
DEFINITION Sequence 1178 from Patent WO0123604.
ACCESSION AX110445
VERSION AX110445.1 GI:13926737
KEYWORDS
SOURCE
ORGANISM Staphylococcus aureus subsp. aureus NCTC 8325.
Staphylococcus aureus subsp. aureus NCTC 8325.
REFERENCE 1 (bases 1 to 2456)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS Bergeron, M. G., Boissinot, M., Huilet, A., m Nard, C., Ouellette, M.,
Picard, F. J. and Roy, P. H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1178 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source location/Qualifiers
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Query Match 100.0%; Score 20; DB 6; Length 2456;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGTGAATATCTTGGC 20
1120 GTTAGTGAATATCTTGGC 1101
Db 1120 GTTAGTGAATATCTTGGC 1101
RESULT 13
SSK8MECA 5596 bp DNA linear BCT 16-JAN-1998
LOCUS S. sciuri meca gene, strain K8 (ATCC700663).
DEFINITION Y13096
ACCESSION Y13096
VERSION Y13096.1 GI:2791919
KEYWORDS meca gene; mecI gene; mecrI gene; NTORE101; NTORE78; ORF142.
SOURCE Staphylococcus sciuri.
ORGANISM Staphylococcus sciuri
REFERENCE 1 (bases 1 to 5596)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS Wu, S., de Lencastre, H. and Tomasz, A.
TITLE Genetic organization of the meca region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus sciuri
JOURNAL J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE 96101461
PUBMED 9440511
REFERENCE 2 (bases 1 to 5596)
Wu, S.

TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences X53818, X54660, L14020, X52593, Y09223.
FEATURES
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1..5596
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HTTISYSSNIDPMWEGIVKQIVLPTVVETMNDKEIEYIILHESHKSHDLIFNQ
LYVFKMIWFMPALYISKTMNDCEKVCDRNLKILNRHEIRYGESILKCSILKS
OHINVAQYLIGFNSNIKERVYIALYDSMPKPNRKRIVAYICGISILLOAPLIS
AHVODKYETNYSYKKNLOLAPYFKGDSFVLYNDRQAVSIYNEPESKORYSPNST
KYITIALAFDONLILSNITTEQOMDKHOIPKERNODONLNSMKYSVMYIENLNKH
EKODEKSTLDLIEGENEISGENENWESSLKISALIEOVNLKNNKONHMDNKAI
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2652..2657
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CDS
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complement(5290..5596)
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BASE COUNT 1991 a 856 c 821 g 1928 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 5596;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGTTGAATATCTTTGCC 20
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Db 3692 GTTAGTTGAATATCTTTGCC 3673
RESULT 14
SSK3MECA2/C 6368 bp DNA linear BCT 16-JAN-1998
LOCUS SSK3MECA2
DEFINITION S.sciuri meca2 gene, strain K3 (HM2).
ACCESSION Y13095
VERSION Y13095.1 GI:2791912
KEYWORDS CTORF261 gene; meca2 gene; mecI gene; mecr1 gene; NTORF101; ORF142.
SOURCE Staphylococcus sciuri.
ORGANISM Staphylococcus sciuri

REFERENCE 1 Bacteria: Firmicutes: Bacillales: Staphylococcus.
AUTHORS Wu, S., de Lencastre, H. and Tomasz, A.
TITLE Genetic organization of the mecA region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus sciuri
JOURNAL J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE 98101461
PUBMED 9440511
REFERENCE 2 (bases 1 to 6368)
AUTHORS Wu, S.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences U14020, X52593, Y09223.
FEATURES
source location/Qualifiers
1..6368
/organism="Staphylococcus sciuri"
/strain="K3 (MM2)"
/sub_species="rodentius"
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LRQDEVKSTLIDLETGENEISGENEINWESSIKTISAIDOVNLKDKKONHFDNKA
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3424..3429
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3448..3453
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3485..3491
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TNGDINRVQNFPEYKEDGMKLDMDHSYIIPGOKDOSIHENLKSERKLDNRNV
ELANTGAYEIGTIPKRVNSKKDYKALIAKELISEDYIQQDMQNVDDTFEPLTKV
KMDVLSYDPKAKFHLPTNPEESBNYPLKATSHLGYGCPINSEHLKQEKYGYDVA
VIGKKGLEKIDRKLLQHEDEGYRTTVTDNSNTIAHTLIRKKRDKDQIQLTIDAKYQK
SLYNNMKNDSYGSTAIPHQTEGLLAVSTPSYDVPYWGMSNEBYNNLTERKKEPLL
NKFOITTPSGSTOKILTAMIGLNKTLDDKTSYKIDGKGMQDKSMGSGRVNRYEVN
GNIDKQALIESSDNIEFARVALSLGSKREKQMKGLGVEDIPSDYPRYNQISKNL
DNEILLADSGYCGEILINPQILISYSALENNGNINPILLDKTKNNKVMKKNISKE
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NTEDAKLTAKYKMKVEKGYELVETVYKPARANQLAMWGYDGIPTDNADKKVHLISO"

BASE COUNT 2230 a 998 c 884 g 2256 t

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YLMNLIQDHRHRIKVRKTRYSINTAKNTLKGIECIYALYKKNRRSLQIYGFSPCHEI
SIMLAS"

BASE COUNT 3099 a 1469 c 1257 g 3222 t
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Query Match 100.0%; Score 20; DB 1; Length 9047;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTAGTTGAATATCTTGCC 20

|||||

Db 4451 GTTAGTTGAATATCTTGCC 4432

Search completed: December 10, 2002, 20:16:52
Job time : 436.756 secs

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OM nucleic - nucleic search, using sw model

Run on : December 10, 2002, 16:03:28 ; Search time 136.911 Seconds
(without alignments)
345.422 Million cell updates/sec

Title: US-09-865-579a-20

Perfect score: 21

Sequence: 1 ttctcttctctctatcaatg 21

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	21	24	ABK85910	Methicillin resist
2	21	100.0	21	24	ABK85920	Methicillin resist
3	21	100.0	36	20	AAK15488	Probe meca938-36 f
4	21	100.0	36	20	AAK15489	Probe meca938-36 f
5	21	100.0	39	24	ABK85927	Methicillin resist
6	21	100.0	59	20	AAK05905	Oligonucleotide pro
7	21	100.0	59	20	AAK15477	Probe meca932-59r
8	21	100.0	89	20	AAK05906	Oligonucleotide pro
9	21	100.0	89	20	AAK15478	Probe meca945-89

C 10	21	100.0	108	20	AAK15487	Probe meca913-1020
C 11	21	100.0	1789	16	AAK04536	Staphylococcus aur
C 12	21	100.0	2007	17	AAK028599	Encodes penicillin
C 13	21	100.0	2007	13	AAK28568	Bacterial antibiotic
C 14	21	100.0	2007	19	AAK68337	Antibiotic binding
C 15	21	100.0	2007	22	AAK76993	Antibiotic resist
C 16	21	100.0	2028	24	ABN92247	Staphylococcus epi
C 17	21	100.0	2110	14	AAK035213	Sequence of the me
C 18	21	100.0	2322	13	AAK025905	pp2', Synthetic.
C 19	21	100.0	2455	16	AAK04538	Staphylococcus aur
C 20	21	100.0	2456	22	AAK01187	Staphylococcus aur
C 21	20	95.2	1467	21	AAK95348	B. subtilis surfac
C 22	19.4	92.4	699	23	AAK51923	Staphylococcus aur
C 23	19.4	92.4	69	23	AAK54834	Staphylococcus aur
C 24	19.4	92.4	781	20	AAK16552	Human gene express
C 25	19.4	92.4	6254	18	AAK74715	Staphylococcus aur
C 26	19.4	92.4	41488	22	AAK87512	Human immunohaema
C 27	18.4	87.6	530	23	ABK52716	Human prostate exp
C 28	18.4	87.6	3650	22	AAK54392	S. epidermidis gen
C 29	18.4	87.6	6888	21	AAK70114	Plasmodium falcipla
C 30	18.4	87.6	32476	22	AAK85314	Human, immune/haema
C 31	18.4	87.6	3353	22	AAK70003	Human adenocarcino
C 32	17.8	84.8	345	24	ABK62597	Human nervous syst
C 33	17.8	84.8	357	22	ABK17944	Human polynucleoti
C 34	17.8	84.8	388	22	AAK191865	Human ovarian tumo
C 35	17.8	84.8	395	22	AAK23887	Human ovarian PCR-
C 36	17.8	84.8	548	22	AAK82444	Human CDNA for an
C 37	17.8	84.8	670	22	AAK56500	Human ovarian PCR-
C 38	17.8	84.8	670	22	AAK24179	Human ovarian PCR-
C 39	17.8	84.8	670	22	AAK82754	Human ovarian tumo
C 40	17.8	84.8	798	21	AAK02444	Human colon cancer
C 41	17.8	84.8	1245	22	AAK33101	Human colon cancer
C 42	17.8	84.8	1301	22	AAK48657	Aspartate/ornithin
C 43	17.8	84.8	1305	21	AAK51562	Arabidopsis thailia
C 44	17.8	84.8	1341	20	AAK61756	B. burgdorferi ant
C 45	17.8	84.8	1350	14	AAK433202	Sequence encoding

ALIGNMENTS

ABK85910	standard; DNA; 21 Bp.
ABK85910:	
16-AUG-2002 (first entry)	
Methicillin resistant Staphylococcus aureus detection primer #10.	
Methicillin resistant Staphylococcus Aureus; MRSA; primer: ss:	
meca; probe.	
Staphylococcus aureus.	
EP1160333-AZ.	
05-DEC-2001.	
29-MAY-2001; 2001EP-0112100.	
29-MAY-2000; 2000UP-0163149.	
09-JUN-2000; 2000UP-0179394.	
(TOY) TOSOH CORP.	
Taya T, Ishiguro T, Saito J;	
WPI; 2002-395832/43.	
New oligonucleotide specific for the meca methicillin-resistance gene,	
useful for cleavage, detection and amplification of the gene or related	

PT mRNA -
 XX
 PS Claim 1; Page 16; 28pp; English.
 CC
 CC This invention relates to oligonucleotides used for cleaving, detecting
 CC and amplifying the meca gene (associated with methicillin resistance in
 CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
 CC a detection method employing an RNA amplification process, using RNA
 CC derived from the meca gene as template. Also disclosed is a detection
 CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
 CC amplification process in the presence of a complementary oligonucleotide
 CC probe labelled with an intercalated fluorescent dye, where complementary
 CC binding of the probe to the RNA transcription product results in a
 CC change in the fluorescent property relative to that of a situation where
 CC a complex formation is absent, and then measuring the fluorescence
 CC intensity of the reaction solution. The oligonucleotides may be used as
 CC primers or probes, for detecting methicillin-resistant *S. aureus* in
 CC clinical samples. They may also be used therapeutically to inhibit RNA
 CC reverse transcription or translation. These oligonucleotides permit
 CC rapid and very sensitive detection/identification of the meca gene, at a
 CC relatively low temperature without the need for heat denaturation of
 CC target RNA. The present sequence represents a methicillin resistant
 CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
 CC
 SO Sequence 21 BP; 3 A; 3 C; 1 G; 14 T; 0 other;
 Query Match 100.0%; Score 21; DB 24; Length 21;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TTTCTTTTCTCTATTATG 21
 Db 1 TTTCTTTTCTCTATTATG 21
 RESULT 2
 ABRK85920
 ID ABRK85920 standard; DNA: 21 BP.
 AC
 AC ABRK85920;
 DT 16-AUG-2002 (first entry)
 XX
 DE Methicillin resistant *Staphylococcus aureus* detection primer #20.
 XX
 KM Methicillin resistant *Staphylococcus aureus*; MRSA; primer; ss;
 KM meca; probe.
 XX
 Staphylococcus aureus.
 EP1160333-A2.
 PD 05-DEC-2001.
 PD 29-MAY-2001; 2001EP-0112100.
 PF
 XX 29-MAY-2000; 2000JP-0163149.
 PR 09-JUN-2000; 2000JP-0179394.
 XX
 XX (TOYU) TOSOH CORP.
 PA
 XX Taya T, Ishiguro T, Saito J;
 PI
 XX WPI: 2002-395832/43.
 DR
 XX New oligonucleotide specific for the meca methicillin-resistance gene,
 PT useful for cleavage, detection and amplification of the gene or related
 PT mRNA -
 XX
 PS Claim 5; Page 19; 28pp; English.
 CC This invention relates to oligonucleotides used for cleaving, detecting
 CC and amplifying the meca gene (associated with methicillin resistance in

CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
 CC a detection method employing an RNA amplification process, using RNA
 CC derived from the meca gene as template. Also disclosed is a detection
 CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
 CC amplification process in the presence of a complementary oligonucleotide
 CC probe labelled with an intercalated fluorescent dye, where complementary
 CC binding of the probe to the RNA transcription product results in a
 CC change in the fluorescent property relative to that of a situation where
 CC a complex formation is absent, and then measuring the fluorescence
 CC intensity of the reaction solution. The oligonucleotides may be used as
 CC primers or probes, for detecting methicillin-resistant *S. aureus* in
 CC clinical samples. They may also be used therapeutically to inhibit RNA
 CC reverse transcription or translation. These oligonucleotides permit
 CC rapid and very sensitive detection/identification of the meca gene, at a
 CC relatively low temperature without the need for heat denaturation of
 CC target RNA. The present sequence represents a methicillin resistant
 CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
 CC
 SO Sequence 21 BP; 3 A; 3 C; 1 G; 14 T; 0 other;
 Query Match 100.0%; Score 21; DB 24; Length 21;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TTTCTTTTCTCTATTATG 21
 Db 1 TTTCTTTTCTCTATTATG 21
 RESULT 3
 AAX15488/C
 ID AAX15488 standard; DNA: 36 BP.
 AC
 AC AAX15488;
 DT 07-MAY-1999 (first entry)
 XX
 DE Probe meca938-36 for detecting an antibiotic resistant meca gene.
 XX
 KM Antibiotic resistant meca gene; transmission; treatment;
 KM methicillin resistant; *Staphylococcus*; probe; ss.
 XX
 OS Synthetic.
 OS *Staphylococcus* sp.
 XX
 PN W09901572-A2.
 PD 14-JAN-1999.
 PD 03-JUL-1998; 98WO-CA00633.
 PF
 XX 22-JUN-1998; 98US-0090276.
 PR 03-JUL-1997; 97US-0051643.
 PR 18-MAY-1998; 98US-0086020.
 XX
 PA (IDBI-) ID BIOMEDICAL CORP.
 XX
 PI Bekkaoui F, Cloney LP;
 DR WPI: 1999-106072/09.
 XX
 XX Method for determining the presence of an antibiotic resistant meca
 PT gene in a sample - using a scissile link containing nucleic acid
 PT probe for antibiotic resistant meca gene
 XX
 PS Example 1; Page 17; 59pp; English.
 CC The present sequence represents a probe used for determining the
 CC presence of an antibiotic resistant meca gene in a biological sample.
 CC The method provides a means for the rapid detection, for both
 CC the prevention of transmission and treatment of, methicillin resistant
 CC *Staphylococcus* species.


```

DT 11-APR-1996 (first entry)
XX
XX Staphylococcus aureus 'meca' protein coding sequence.
DE
XX methicillin-resistant Staphylococcus aureus; MRSA; 'meca' protein;
KM antibiotic resistance; ds.
XX
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
XX CDS 1..1608
XX /tag= a
XX /product= 'mecA' protein
XX
XX JP07209294-A.
XX
XX 11-AUG-1995.
XX
XX 10-JAN-1994; 94JP-0012226.
XX
XX 10-JAN-1994; 94JP-0012226.
XX
XX 10-JAN-1994; 94JP-0012226.
XX
XX (DENK-) DENKA SEIKEN KK.
XX (KAWA/) KAWANO M.
XX (MITU) MITSUBISHI CHEM CORP.
XX
XX WPI; 1995-313917/41.
XX P-PSDB; AAR80035.
XX
XX New 'mecA' protein and DNA encoding it - used for the detection of
XX methicillin-resistant Staphylococcus aureus
XX
XX Claim 5; Page 11-13; 15pp; Japanese.
XX
XX The present sequence codes for the 'mecA' protein which controls
XX methicillin resistance in methicillin-resistant Staph. aureus. The
XX 'mecA' protein (mol. wt. 40000) is useful for preparation of
XX an antiserum specific for MRSA, thereby allowing methicillin-resistant
XX and methicillin-sensitive strains to be distinguished. The coding
XX sequence was obtained by PCR amplification of the mecA sequence
XX (see AAT04538) using primers AAT04537 and AAT04539.
XX N.B. In the sequence listing of the patent specification, the
XX sequence length is stated to be 1785 bp.
XX
XX Sequence 1789 BP; 735 A; 263 C; 302 G; 489 T; 0 other;
XX
XX Query Match 100.0%; Score 21; DB 16; Length 1789;
XX Best Local Similarity 100.0%; Pred. No. 81;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTTTCTTTTCTCTATTATG 21
XX |||||||||||||||||||
XX 556 TTTTCTTTTCTCTATTATG 536
XX
XX RESULT 12
XX AAQ28599/c
XX ID AAQ28599 standard; DNA: 2007 BP.
XX
XX AAQ28599;
XX
XX 19-FEB-1993 (first entry)
XX
XX Encodes penicillin binding protein PBP2A-27R.
XX
XX Penicillin; antibiotic; bacteria; methicillin; staphylococci;
XX soluble; chelating peptide; MRS infection; methicillin resistant;
XX strain.
XX
XX Staphylococcus aureus strain 27R.
XX
XX Key Location/Qualifiers
XX CDS 1..2007
XX

```

```

XX
XX /tag= a
XX
XX EP505151-A.
XX
XX 23-SEP-1992.
XX
XX 18-MAR-1992; 92EP-0302298.
XX
XX 19-MAR-1991; 91US-0672704.
XX
XX (ELL) LILLY & CO ELL.
XX
XX Blaszcak LC, Skatrud PL, Smith MC, Wu CYE;
XX WPI; 1992-318034/39.
XX
XX Polynucleotide cpd. encoding PBP 2A-27R protein or its deriv. -
XX contains PBP isolated from Staphylococcus aureus and is used to
XX treat methicillin resistant staphylococci
XX
XX Disclosure; Page 14; 101pp; English.
XX
XX This sequence encodes a PBP2a penicillin binding protein isolated
XX from S. aureus strain 27R. A cDNA library was constructed from
XX S. aureus DNA in lambda phage EMBL3. Packaging extracts from this were
XX then used to infect E. coli CJ236. Plaques were screened for the
XX presence of the mecA-27R gene by a probe produced by PCR amplification
XX of the mecA gene using primers Q28600.1. Positive plaques were purified
XX and digested with HindIII, and this fragment digested with XbaI and
XX cloned into M13mp18 and M13mp19 for sequencing.
XX
XX Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
XX
XX Query Match 100.0%; Score 21; DB 13; Length 2007;
XX Best Local Similarity 100.0%; Pred. No. 81;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTTTCTTTTCTCTATTATG 21
XX |||||||||||||||||||
XX 955 TTTTCTTTTCTCTATTATG 935
XX
XX RESULT 13
XX AAT28568/c
XX ID AAT28568 standard; DNA: 2007 BP.
XX
XX AAT28568;
XX
XX 01-APR-1997 (first entry)
XX
XX Bacterial antibiotic resistance gene, mecA, probe.
XX
XX Detection; probe; amplification primer; bacterial pathogen; pneumonia;
XX Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
XX Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
XX Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
XX Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
XX Haemophilus influenzae; Moraxella catarrhalis; septicemia; meningitis;
XX infection; intra-abdominal infection; skin infection;
XX bacterial resistance; beta-lactam antibiotic; ds.
XX
XX Synthetic.
XX
XX WO9608582-A2.
XX
XX 21-MAR-1996.
XX
XX 12-SEP-1995; 95WO-CA00528.
XX
XX 12-SEP-1994; 94US-0304732.
XX
XX (BERG/) BERGERON M G.
XX (OUEL/) OUELLETTE M.
XX

```

PA	(ROY/P/ROY P. H.
PI	Bergeron MG, Ouellette M, Roy PH;
XX	WPI: 1996-179953/18.
DR	
XX	
XX	Method for the detection of bacterial species using probes and
PT	primers - allows detection and quantification of antibiotic
PT	resistant bacteria in patients, the environment and food
XX	
PS	Claim 91; Page 144-145; 216pp; English.
XX	
CC	The sequences given in AAT28560-76 represent fragments derived from
CC	bacterial antibiotic resistance genes which were used as probes in the
CC	method of the invention for the detection of bacterial species in a
CC	sample. The method of the invention comprises using probes and/or
CC	amplification primers which are specific, ubiquitous and sensitive for
CC	determining the presence and/or amount of nucleic acids from selected
CC	bacterial species in any sample, where the bacterial nucleic acid
CC	comprises a selected target region hybridisable with the probes or
CC	primers. The method comprises contacting the sample with the probes
CC	or primers or amplification products as and indication of the presence
CC	and/or amount of the bacterial species. This method may be used to
CC	detect commonly encountered bacterial pathogens, e.g. <i>Escherichia coli</i> ,
CC	<i>Klebsiella pneumoniae</i> , <i>Pseudomonas aeruginosa</i> , <i>Proteus mirabilis</i> ,
CC	<i>Streptococcus pneumoniae</i> , <i>Staphylococcus aureus</i> , <i>Staphylococcus</i>
CC	<i>epidermidis</i> , <i>Enterococcus faecalis</i> , <i>Staphylococcus saprophyticus</i> ,
CC	<i>Streptococcus pyogenes</i> , <i>Haemophilus influenzae</i> and <i>Moraxella</i>
CC	<i>catarrhalis</i> . These bacterial species are associated with approx. 90% of
CC	urinary tract infections and with a high percentage of other severe
CC	infections including septicæmia, meningitis, pneumonia, intra-abdominal
CC	infections, skin infections and other severe respiratory tract
CC	infections. The method may also be used to evaluate a bacterial
CC	resistance to beta-lactam antibiotics.
XX	
SO	Sequence 2007 BP: 855 A: 270 C: 341 G: 541 T: 0 other:
	Query Match 100.0%; Score 21; DB 17; Length 2007;
	Host Local Similarity 100.0%; Prev. NO. 81;
	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
0Y	1 TTTTCTTTTCTCTATTATG 21
DB	955 TTTTCTTTTCTCTATTATG 935
	RESULT 14
	AAV68337/C
C	AAV68337 standard; DNA: 2007 BP.
XX	
AC	AAV68337:
XX	
DT	21-JUN-1999 (first entry)
XX	
DE	Penicillin binding protein PBP2A mecA-27R gene of <i>S. aureus</i> 27R.
XX	
KW	penicillin binding protein: PBP2A-27R; mecA-27R gene;
KW	methicillin resistance; antibiotic assay; purification; ss.
XX	
OS	Staphylococcus aureus.
XX	
PN	KIP875578-A2.
XX	
PD	04-NOV-1998.
XX	
PF	18-MAR-1992; 92EP-0302298.
XX	
PR	19-MAR-1991; 91US-0672704.
XX	
PA	(F.I.L.) LILLY & CO. Ltd.
XX	
BI	Biasczak LC, Skatrud PL, Smith MC, Wu CE;

XX	WP1: 1998-559443/748.
DR	P-PsDB; AAM81149.
XX	New Staphylococcus aureus soluble penicillin-binding proteins and
PT	their derivatives - useful for screening for compounds effective
PT	against methicillin resistant organisms
XX	
PS	Disclosure; Page 14-16: 97pp; English.
XX	
CC	This meca-27r gene encodes penicillin binding protein 2A (PBP2A-27r)
CC	responsible for the methicillin resistance of Staphylococcus aureus
CC	strain 27r. The invention provides new PBPs of formula SP-L-PBP2As,
CC	where: SP is 0 or a signal peptide (preferably from the ampc, ompA or
CC	beta-lactamase gene product); L is Met-Val or a compound of formula
CC	Met-Gly-Cp-(Pro)n-PBP2As, where Cp = 0 or a chelating peptide (see
CC	AAM81151-58) of formula (His)x-(A)y-(His)z and A-an amino acid,
CC	x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above
CC	polypeptide where each monomer unit is the same or different; Pro
CC	is proline, n = 0 or 1; and PBP2As is soluble PBP2A-27r protein (see
CC	AAM81159-62). Also claimed are polynucleotides encoding specific
CC	soluble PBP2A compounds. The new PBP2A-27r proteins are useful for
CC	assaying for agents useful as antibiotics against methicillin
CC	resistant Staphylococcus strains by creating a kinetically inert
CC	complex between a support-immobilised transition ion and a modified
CC	soluble PBP2A protein comprising a chelating agent, which screens
CC	for agents which bind to PBP2A proteins (disclosed). Soluble forms
CC	of PBP2A-27r protein facilitate crystallisation as they lack their
CC	transmembrane association region, and so are useful for x-ray
CC	crystallography studies of the protein, assisting in the design of
CC	antibiotic compounds against methicillin resistant Staphylococcus
CC	strains (disclosed). The chelating peptide operably linked to the
CC	BPA2-27r proteins is useful for purifying PBPs.
XX	
SO	Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
	Query Match 100.0%; Score 21; DB 19; Length 2007;
	Best Local Similarity 100.0%; Pred. NO. 81;
	Ma.ches 21; Conservative 0; Mismatches 0; Indels 0; Gaps
OY	1 TTTTCTTTTTTCGTATTAATG 21
	TTTTTTTTTTTTTTTT
Dd	955 TTTTCTTTTCTCATTAATG 935
	RESULT 15
	ABA76993/C
ID	ABA76993 standard: DNA; 2007 BP.
XX	
AC	ABA76993:
XX	
DT	28-JAN-2002 (first entry)
XX	
DE	Antibiotic resistance detection polynucleotide SEQ ID NO 169.
XX	
KM	Detection: bacterial species; animal; food; environment;
KW	antibiotic resistance; ds.
XX	
OS	Unidentified.
XX	
FN	NZ501596-A.
XX	
PD	29-JUN-2001.
XX	
PP	12-SEP-1995; 95NZ-0501596.
XX	
PR	12-SEP-1995; 95NZ-0501596.
XX	
PA	(IDI1-) IDI INFECTIO DIAGNOSTIC INC.
XI	Bergeron MG, Ouellette M, Roy PH;
XX	
DR	WP1: 2001-615034/71.

XX Method for detecting target bacterial species in a sample, comprises
 PT detecting the presence or amount of bacterial nucleic acid amplified by
 PT a primer derived from bacterial DNA, specific for the target bacterial
 PT species -

PS Claim 16; Page 159-160; 168pp; English.

XX
 CC The invention relates to detecting target bacterial species suspected to
 CC be present in a sample, comprising contacting nucleic acids of target
 CC bacterial species with an amplification primer pair derived from a
 CC bacterial DNA fragment (ABA/6825-ABA/6861) specific for the target
 CC bacterial species but ubiquitous for different strains, amplifying the
 CC nucleic acid and detecting the presence or amount of an amplified
 CC sequence as an indication of the presence or amount of the target
 CC bacterial species. The invention includes primers and probes
 CC (ABA/6862-ABA/6984) against the target bacterial species, especially
 CC *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *P. mirabilis*, *S. pneumoniae*,
 CC *S. aureus*, *S. epidermidis*, *E. faecalis*, *S. saprophyticus*, *S. pyogenes*,
 CC *H. influenzae*, *M. catarrhalis* and/or group A *Streptococci* producing
 CC exotoxin A gene spe A, suspected to be present in a sample which is
 CC obtained from human patients, animals, environment or food, and which
 CC consists of one or more bacterial colonies. Oligonucleotide
 CC probes and primers complementary to the bacterial genes encoding
 CC resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aacB,
 CC aacC1, aacC2, aacC3, aacA4, mecA, vanA, vanH, vanX, satA, aacA-apbD, vat,
 CC vga, msrA, sul and/or int (ABA/6985-ABA/7001) are also useful to identify
 CC commonly encountered and clinically important resistance genes. The
 CC invention provides a rapid method of bacterial identification that can be
 CC achieved, which reduces the time currently required for the
 CC identification of pathogens in the clinical laboratory.

XX
 SQ Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other:

Query Match 100.0%; Score 21; DB 22; Length 2007;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTATG 21
 ||||||||||||||||

Db 955 TTTCTTTTCTCTATTATG 935

Search completed: December 10, 2002, 17:32:32
 Job time : 138.911 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 ; Search time 28.6257 Seconds
(without alignments)
224,980 Million cell updates/sec

Title: US-09-865-579A-20

Perfect score: 21
Sequence: 1 tttctttcttctatctaatg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2.6/prodata1/1na/5A_COMB.seq: *
2: /cgn2.6/prodata1/1na/5B_COMB.seq: *
3: /cgn2.6/prodata1/1na/6A_COMB.seq: *
4: /cgn2.6/prodata1/1na/6B_COMB.seq: *
5: /cgn2.6/prodata1/1na/PCTUS_COMB.seq: *
6: /cgn2.6/prodata1/1na/backfile1.seq: *

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	21	100.0	2007	2	US-08-743-637B-169 Sequence 169, App
C 2	21	100.0	2007	3	US-08-526-840B-169 Sequence 169, App
C 3	17.8	100.0	2028	4	US-09-134-001C-1710 Sequence 1710, Ap
C 4	17.8	84.8	1350	2	US-08-244-205-1 Sequence 1, Appl1
C 5	17.8	84.8	1350	5	PCT-US92-10284-1 Sequence 1, Appl1
C 6	17.4	82.9	2162	2	US-08-870-518-5 Sequence 5, Appl1
C 7	17	81.0	29	3	US-09-109-857-4 Sequence 4, Appl1
C 8	17	81.0	29	3	US-09-109-857-5 Sequence 5, Appl1
C 9	17	81.0	1665	4	US-09-221-017B-1017 Sequence 1017, Ap
C 10	16.8	80.0	432	4	US-09-134-001C-104 Sequence 104, App
C 11	16.8	80.0	583	4	US-09-385-982-86 Sequence 86, Appl
C 12	16.8	80.0	696	4	US-09-134-001C-760 Sequence 760, Appl
C 13	16.8	80.0	1143	4	US-09-134-001C-993 Sequence 993, App
C 14	16.8	80.0	1875	1	US-08-286-325A-1 Sequence 1, Appl1
C 15	16.8	80.0	2667	1	US-09-134-001C-195 Sequence 195, App
C 16	16.8	80.0	3234	4	US-08-286-325A-7 Sequence 7, Appl1
C 17	16.8	80.0	9713	1	US-08-961-527-43 Sequence 43, Appl1
C 18	16.4	78.1	2770	4	US-08-426-509A-5 Sequence 5, Appl1
C 19	16.4	78.1	2770	5	PCT-US95-05008-5 Sequence 5, Appl1
C 20	16.4	78.1	7607	1	US-08-222-616-19 Sequence 19, Appl1
C 21	16.4	78.1	7607	4	US-08-446-648-19 Sequence 19, Appl1
C 22	16.4	78.1	7607	5	PCT-US95-04228-19 Sequence 19, Appl1
C 23	16.4	78.1	84495	1	US-09-797-906-3 Sequence 3, Appl1
C 24	16.2	77.1	474	1	US-08-412-614-93 Sequence 93, Appl1
C 25	16.2	77.1	474	1	US-08-635-761-93 Sequence 93, Appl1
C 26	16.2	77.1	474	4	US-09-312-520-93 Sequence 93, Appl1
C 27	16.2	77.1	476	1	US-08-412-614-94 Sequence 94, Appl1

C 28	16.2	77.1	476	2	US-08-635-761-94 Sequence 94, Appl1
C 29	16.2	77.1	476	4	US-09-312-520-94 Sequence 94, Appl1
C 30	16.2	77.1	547	3	US-09-188-930-14 Sequence 14, Appl1
C 31	16.2	77.1	699	4	US-09-328-111-190 Sequence 190, App
C 32	16.2	77.1	759	4	US-09-134-001C-2807 Sequence 2807, Ap
C 33	16.2	77.1	1051	4	US-09-063-743-4 Sequence 4, Appl1
C 34	16.2	77.1	1051	4	US-09-590-540-4 Sequence 4, Appl1
C 35	16.2	77.1	1056	2	US-08-929-417-1 Sequence 1, Appl1
C 36	16.2	77.1	2173	6	5168051-10 Patent No. 5168051
C 37	16.2	77.1	2338	3	US-09-058-489-37 Sequence 37, Appl1
C 38	16.2	77.1	4235	4	US-09-342-681C-18 Sequence 18, Appl1
C 39	16.2	77.1	4792	4	US-09-189-462-5 Sequence 5, Appl1
C 40	16.2	77.1	5113	3	US-08-973-273-2 Sequence 2, Appl1
C 41	16.2	77.1	5715	3	US-09-107-847-1 Sequence 1, Appl1
C 42	16.2	77.1	6755	3	US-08-931-999-4 Sequence 4, Appl1
C 43	16	76.2	35828	4	US-09-449-218D-17 Sequence 17, Appl1
C 44	15.8	75.2	420	4	US-09-641-638-331 Sequence 331, App
C 45	15.8	75.2	672	4	US-09-134-001C-1570 Sequence 1570, Ap

ALIGNMENTS

RESULT 1
US-08-743-637B-169/C
Sequence 169, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: OUELLETTE & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586, 90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0% Score 21: DB 2: Length 2007:

ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: PCF3
FEATURE:
NAME/KEY: CDS
LOCATION: 46..1206
US-08-244-205-1

Query Match 84.8%; Score 17.8; DB 2; Length 1350;
Best Local Similarity 90.5%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTTCTTTTCTCTATTATG 21
|||||
DB 1308 TTTCTTTTCTTTATTATG 1328

RESULT 5
PCT-US92-10284-1

Sequence 1, Application PC/TUS9210284

GENERAL INFORMATION:

APPLICANT: Browse, John, Kinney, Anthony J.,
APPLICANT: Pierce, John, Wierzbicki, Anna M.,
APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
TITLE OF INVENTION: Fatty Acid Desaturase Genes
TITLE OF INVENTION: from plants
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: Macintosh System, 6.0

SOFTWARE: Microsoft Word, 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10284

FILING DATE: 19921203

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/804,259

FILING DATE: 4 DECEMBER 1991

ATTORNEY/AGENT INFORMATION:

NAME: Floyd, Linda A.

REGISTRATION NUMBER: 33,692

REFERENCE/DOCKET NUMBER: BB-1036-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 992-4929

TELEFAX: (302) 892-7949

TELEFX: 835420

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1350 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Arabidopsis thaliana IMMEDIATE SOURCE:

IMMEDIATE SOURCE:

CLONE: PCF3

FEATURE:

NAME/KEY: CDS

LOCATION: 46..1206

PCT-US92-10284-1

Query Match 84.8%; Score 17.8; DB 5; Length 1350;

Best Local Similarity 90.5%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTTCTTTTCTCTATTATG 21
|||||
DB 1308 TTTCTTTTCTTTATTATG 1328

RESULT 6

US-08-870-518-5/C

Sequence 5, Application US/08870518

Patent No. 5925366

GENERAL INFORMATION:

APPLICANT: Davis, Roger J.

APPLICANT: Galcheva-Gargova, Zoya

TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX

TITLE OF INVENTION: PROTEINS AND USES THEREOF

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSER: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/870,518

FILING DATE: 06-JUN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/019,219

FILING DATE: 06-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Passe, Peter J.

REGISTRATION NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 04020/102001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEFX: 200154

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 2162 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 89...1465

US-08-870-518-5

Query Match 82.9%; Score 17.4; DB 2; Length 2162;

Best Local Similarity 94.7%; Pred. No. 1.8e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCTTTTCTCTATTATG 19
|||||
DB 1978 TTTCTTTTCTTTATTATG 1960

RESULT 7

US-09-109-957-4/C

Sequence 4, Application US/09109957

Patent No. 6136533

GENERAL INFORMATION:

APPLICANT: Bekkaoui, Faouzi

APPLICANT: Modrusan, Zora D.

APPLICANT: Pische, Isabelle A.

APPLICANT: Duck, Peter D.

```
; APPLICANT: Cloney, Lynn P.
; APPLICANT: Wong, Alfred C.K.
; TITLE OF INVENTION: ADDITIVES FOR USE IN CYCLING PROBE REACTIONS
; FILE REFERENCE: 480094.419
; CURRENT APPLICATION NUMBER: US/09/109,957
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Solid Phase Synthesis
US-09-109-957-4

Query Match          81.0%: Score 17; DB 3; Length 29;
Best Local Similarity 100.0%: Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

f 1 TTTTCTTTTCTCTATT 17
   |||||
Db 17 TTTCTTTTCTCTATT 1

RESULT 8
US-09-109-957-5
; Sequence 5, Application US/09109957
; Patent No. 6136533
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Modrusan, Zora D.
; APPLICANT: Pische, Isabelle A.
; APPLICANT: Duck, Peter D.
; APPLICANT: Cloney, Lynn P.
; APPLICANT: Wong, Alfred C.K.
; TITLE OF INVENTION: ADDITIVES FOR USE IN CYCLING PROBE REACTIONS
; FILE REFERENCE: 480094.419
; CURRENT APPLICATION NUMBER: US/09/109,957
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Solid Phase Synthesis
US-09-109-957-5

Query Match          81.0%: Score 17; DB 3; Length 29;
Best Local Similarity 100.0%: Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTTCTTTTCTCTATT 17
    |||||
Db 13 TTTTCTTTTCTCTATT 29

RESULT 9
US-09-221-017B-1017/c
; Sequence 1017, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
```

```
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Moorov, Gladys H.
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1017:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1665 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1...1665
US-09-221-017B-1017

Query Match          81.0%: Score 17; DB 4; Length 1665;
Best Local Similarity 100.0%: Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TTTCTTTTCTCTATTA 18
   |||||
Db 311 TTTCTTTTCTCTATTA 295

RESULT 10
US-09-134-001C-104/c
; Sequence 104, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
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SEO ID NO 104
LENGTH: 432
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-104

Query Match 80.0%; Score 16.8; DB 4; Length 432;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 TTTCTTTTCTCTATTAT 20
11111111111111111111
Db 188 TTCTCTTTTCTCTAATAAT 169

RESULT 11
US-09-385-982-86/C
Sequence 86, Application US/09385982
Patent No. 6262334
GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSeq for Windows Version 3.0
SEO ID NO 86
LENGTH: 583
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(583)
OTHER INFORMATION: n = A,T,C or G
US-09-385-982-86

Query Match 80.0%; Score 16.8; DB 4; Length 583;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 TTTCTTTTCTCTATTAT 20
11111111111111111111
Db 360 TTTTCTTTTCTCTTAAAT 341

RESULT 12
US-09-134-001C-760/C
Sequence 760, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: CTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEO ID NO 760
LENGTH: 696
TYPE: DNA
ORGANISM: Staphylococcus epidermidis

US-09-134-001C-760

Query Match 80.0%; Score 16.8; DB 4; Length 696;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 TTTCTTTTCTCTATTAT 20
11111111111111111111
Db 488 TTTCTTTTCTTTATCAAT 469

RESULT 13
US-09-134-001C-993/C
Sequence 993, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: CTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEO ID NO 993
LENGTH: 1143
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-993

Query Match 80.0%; Score 16.8; DB 4; Length 1143;
Best Local Similarity 90.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 1 TTTCTTTTCTCTATTAT 20
11111111111111111111
Db 533 TTTCTTTTCTTTATTAGT 514

RESULT 14
US-08-286-325A-1/C
Sequence 1, Application US/08286325A
Patent No. 5658770
GENERAL INFORMATION:
APPLICANT: PREVOTIS, Fabien
APPLICANT: REMY, Elisabeth
TITLE OF INVENTION: Nucleic acid sequence and plasmids
TITLE OF INVENTION: Comprising at least one phage resistance mechanism, bacteria in which they are present, and their use
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: BACON & THOMAS
STREET: 625 Slaters Lane - Fourth floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,325A
FILING DATE: 04-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 09 777
FILING DATE: 09-AUG-1993

```

; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/BDL/
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-1080
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1875 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Lactococcus lactis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 202..1821
; -08-286-325A-1

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Query Match      80.0%; Score 16.8; DB 1; Length 1875;
Best Local Similarity 90.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 1 TTTTCCTTTCTCTATTAAAT 20
    ||||| ||||| |||||
DB 988 TTTTATTCTCTCATTAAT 969

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RESULT 15
US-09-134-001C-195/c
; Sequence 195, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucelte-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: CTC-007
; CURRENT APPLICATION NUMBER: US/09/ 4,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 195
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-195

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Query Match      80.0%; Score 16.8; DB 4; Length 2667;
Best Local Similarity 90.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 1 TTTTCCTTTCTCTATTAAAT 20
    ||||| ||||| |||||
DB 2603 TTTTCTTTCTCATTAAT 2584

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Search completed: December 10, 2002, 22:54:23
 Job time : 30.7507 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 ; Search time 27.2179 Seconds
(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-20

Perfect score: 21

Sequence: 1 tttctttctctattatg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
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2	21	100.0	21	10	US-09-865-579A-20
3	21	100.0	39	10	US-09-865-579A-27
4	21	100.0	2007	10	US-09-452-599-169
5	19.4	92.4	699	10	US-09-815-242-4505
6	19.4	92.4	699	10	US-09-815-242-8471
7	18.4	87.6	2000	9	US-09-938-842A-4244
8	17.8	84.8	395	10	US-09-777-564-68
9	17.8	84.8	548	10	US-09-813-358-124
10	17.8	84.8	670	10	US-09-777-564-360
11	17.8	84.8	2000	9	US-09-938-842A-4081
12	17.8	84.8	2000	9	US-09-938-842A-4149
13	17.4	82.9	403	10	US-09-867-701-2314
14	17.4	82.9	21990	9	US-09-942-429A-9
15	17.4	82.9	1503841	9	US-09-946-807-1
16	17.4	82.9	1503841	10	US-09-795-668-1
17	17.4	82.9	1503841	10	US-09-795-668-1
18	17	81.0	1431	10	US-09-974-300-2891
19	17	81.0	5840	10	US-09-070-927A-31

C	20	16.8	80.0	286	10	US-09-880-107-2012	Sequence 2012, Ap
C	21	16.8	80.0	380	9	US-09-933-797-438	Sequence 438, Ap
C	22	16.8	80.0	393	10	US-09-878-574-1244	Sequence 1244, Ap
C	23	16.8	80.0	453	10	US-09-880-107-2589	Sequence 2589, Ap
C	24	16.8	80.0	496	10	US-09-783-590-12266	Sequence 12266, A
C	25	16.8	80.0	483	9	US-09-954-531-1115	Sequence 1115, Ap
C	26	16.8	80.0	496	10	US-09-964-824A-149	Sequence 149, Ap
C	27	16.8	80.0	1097	10	US-09-974-300-2653	Sequence 2653, Ap
C	28	16.8	80.0	1516	10	US-09-925-302-291	Sequence 291, Ap
C	29	16.8	80.0	1571	9	US-09-981-353-86	Sequence 86, Ap
C	30	16.8	80.0	2000	9	US-09-938-842A-4131	Sequence 4131, Ap
C	31	16.8	80.0	21761	10	US-09-764-847-1680	Sequence 1680, Ap
C	32	16.8	80.0	180216	10	US-09-835-232-6	Sequence 6, Ap
C	33	16.8	80.0	326014	10	US-09-731-231A-3	Sequence 3, Ap
C	34	16.8	80.0	465237	10	US-09-933-267A-1	Sequence 1, Ap
C	35	16.8	78.1	245	10	US-09-728-445-790	Sequence 790, Ap
C	36	16.4	78.1	516	10	US-09-815-242-4261	Sequence 4261, Ap
C	37	16.4	78.1	522	10	US-09-864-761-12370	Sequence 12370, A
C	38	16.4	78.1	690	10	US-09-815-242-8293	Sequence 8293, Ap
C	39	16.4	78.1	862	9	US-09-938-842A-3058	Sequence 3058, Ap
C	40	16.4	78.1	1175	10	US-09-070-927A-660	Sequence 660, Ap
C	41	16.4	78.1	2000	9	US-09-938-842A-3106	Sequence 3106, Ap
C	42	16.4	78.1	2508	10	US-09-070-927A-623	Sequence 623, Ap
C	43	16.4	78.1	2770	10	US-09-977-269-5	Sequence 5, Ap
C	44	16.4	78.1	2863	10	US-09-954-456-1631	Sequence 1631, Ap
C	45	16.4	78.1	4187	10	US-09-764-855-252	Sequence 252, Ap

ALIGNMENTS

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RESULT 1
US-09-865-579A-10
; Sequence 10, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Yoshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865, 579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to meca gene
US-09-865-579A-10

Query Match      100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTTCTTTCTCTATTATG 21
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DB 1 TTTTCTTTCTCTATTATG 21

RESULT 2
US-09-865-579A-20
; Sequence 20, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
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; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; -09-865-579A-20

Query Match          100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTATG 21
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Db 1 TTTCTTTTCTCTATTATG 21

RESULT 3
US-09-865-579A-27
; Sequence 27, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-865-579A-27

Query Match          100.0%; Score 21; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTCTTTTCTCTATTATG 21

RESULT 4
US-09-452-599-169/c
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
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; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: To Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match          100.0%; Score 21; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTATG 21
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Db 955 TTTCTTTTCTCTATTATG 935

RESULT 5
US-09-815-242-4505/c
; Sequence 4505, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4505
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4505

Query Match          92.4%; Score 19.4; DB 10; Length 699;
Best Local Similarity 95.2%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 TTTTCTTTTCTCTATTATG 21
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DB 491 TTTTCTTTTCTCTATTATG 471

RESULT 6
US-09-815-242-8471/c

; Sequence 8471, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsson, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8471

LENGTH: 699

TYPE: DNA

ORGANISM: Staphylococcus aureus

FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(699)
US-09-815-242-8471

Query Match 92.4%; Score 19.4; DB 10; Length 699;
Best Local Similarity 95.2%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTTCTTTTCTCTATTATG 21
|||||
DB 491 TTTTCTTTTCTCTATTATG 471

RESULT 7
US-09-938-842A-4244

; Sequence 4244, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SRIPI300-3

CURRENT FILING DATE: 2001-08-24

CURRENT APPLICATION NUMBER: US/09/938,842A

PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

US-09-938-842A-4244

US-09-938-842A-4244

US-09-938-842A-4244

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US-09-938-842A-4244

US-09-938-842A-4244

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 4244

LENGTH: 2000

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-4244

US-09-938-842A-4244

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US-09-938-842A-4244

US-09-938-842A-4244

US-09-938-842A-4244

US-09-938-842A-4244

FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(548)
OTHER INFORMATION: n = A,T,C or G
US-09-813-358-124

Query Match Best Local Similarity 84.8%; Score 17.8; DB 10; Length 548;
Best Local Similarity 90.5%; Pred. No. 3.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Caps 0;

OY 1 TTTTCTTTTCTCTATTATG 21
|||||
Db 8 TTTTCTTTTCTCTAGTATG 28

RESULT 10
US-09-777-564-360/C
Sequence 360, Application US/09777564
Patent No. US20020022591A1
GENERAL INFORMATION:
APPLICANT: Aligate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.493
CURRENT APPLICATION NUMBER: US/09/777.564
CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
SOFTWARE: FastSeq for Window Version 4.0
SEQ ID NO 360
LENGTH: 670
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(670)
OTHER INFORMATION: n = A,T,C or G
US-09-777-564-360

Query Match Best Local Similarity 84.8%; Score 17.8; DB 10; Length 670;
Best Local Similarity 90.5%; Pred. No. 3.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Caps 0;

OY 1 TTTTCTTTTCTCTATTATG 21
|||||
Db 177 TTTTCTTTTCTCTACATG 157

RESULT 11
US-09-938-842A-4081
Sequence 4081, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SRRP1300-3
CURRENT APPLICATION NUMBER: US/09/938.842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4081
LENGTH: 2000
TYPE: DNA
ORGANISM: Arabidopsis thaliana

US-09-938-842A-4081

Query Match Best Local Similarity 84.8%; Score 17.8; DB 9; Length 2000;
Best Local Similarity 90.5%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Caps 0;

OY 1 TTTTCTTTTCTCTATTATG 21
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Db 728 TTTTCTTTTCTCTAGTATG 748

RESULT 12
US-09-938-842A-4149/C
Sequence 4149, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SRRP1300-3
CURRENT APPLICATION NUMBER: US/09/938.842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4149
LENGTH: 2000
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-4149

Query Match Best Local Similarity 84.8%; Score 17.8; DB 9; Length 2000;
Best Local Similarity 90.5%; Pred. No. 3.8e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Caps 0;

OY 1 TTTTCTTTTCTCTATTATG 21
|||||
Db 1890 TTTTCTTTTCTCAATTAAG 1870

RESULT 13
US-09-867-701-2314/C
Sequence 2314, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Agiate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867.701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2314
LENGTH: 403
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(403)
OTHER INFORMATION: n = A,T,C or G
US-09-867-701-2314

Query Match Best Local Similarity 82.9%; Score 17.4; DB 10; Length 403;

Best Local Similarity 94.7%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTAA 19
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Db 210 TTTCTTTTCTCTATTAA 192

RESULT 14

US-09-942-429A-9
; Sequence 9, Application US/09942429A
; Patent No. US20020165208A1
; GENERAL INFORMATION:
; APPLICANT: JORGE H. CAPEVILLA, MICHAEL WATERMAN, AND VIJAKUMAR HOLLA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO
; FILE REFERENCE: 22000.011002
; CURRENT APPLICATION NUMBER: US/09/942,429A
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/228,947
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 21990
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NO. US20020165208A1e -
; NAME/KEY: misc_feature
; LOCATION: (1)...(21990)
; OTHER INFORMATION: n = 9, a, c or t(u)
US-09-942-429A-9

Query Match 82.9%; Score 17.4; DB 9; Length 21990;
Best Local Similarity 94.7%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTAA 19
||| ||||| ||||| |||||
Db 6217 TTTCTTTTCTCTATTAA 6235

RESULT 15

US-09-946-807-1/c
; Sequence 1, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Guilcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/946,807
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r-g or a
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)

OTHER INFORMATION: y-t/u or c

FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: m-a or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: k-g or t/u
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: s-g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: w-a or t/u
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: b-g or c or t/u
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: d-a or g or t/u
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: h-a or c or t/u
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: v-a or g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: n-a or g or c or t/u
US-09-946-807-1

Query Match 82.9%; Score 17.4; DB 9; Length 1503841;
Best Local Similarity 94.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTTCTTTTCTCTATTAA 20
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Db 1457430 TTTCTTTTCTCTATTAA 1457412

Search completed: December 11, 2002, 06:07:18
Job time : 277.218 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 ; Search time 25.9218 Seconds
(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-24

Perfect score: 20
Sequence: 1 tcattgctgtaattttt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

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Maximum Match 100%

Listing first 45 summaries

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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NMW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	10	US-09-865-579A-14
2	20	100.0	20	10	US-09-865-579A-24
3	20	100.0	20	10	US-09-452-599-169
4	18.4	92.0	648	12	US-10-001-843-114
5	18.4	92.0	928	12	US-10-001-843-115
6	16.8	84.0	32191	10	US-09-764-864-1678
7	16.8	84.0	640681	10	US-09-790-988-1
8	16	80.0	963	10	US-09-815-242-4716
9	16	80.0	966	10	US-09-815-242-8596
10	16	80.0	966	10	US-09-815-242-8623
11	16	80.0	640681	10	US-09-790-988-1
12	15.8	79.0	124	10	US-09-783-590-6025
13	15.8	79.0	187	10	US-09-983-965-4889
14	15.8	79.0	191	10	US-09-783-590-5750
15	15.8	79.0	345	10	US-09-983-965-4863
16	15.8	79.0	364	10	US-09-764-869-2135
17	15.8	79.0	366	10	US-09-969-373-801
18	15.8	79.0	677	10	US-09-828-644-24
19	15.8	79.0	754	10	US-09-815-242-3149

20	15.8	79.0	810	10	US-09-974-300-5530	Sequence 5530, Ap
21	15.8	79.0	1981	9	US-09-258-0318-57	Sequence 57, Appl
22	15.8	79.0	2009	10	US-09-764-869-2134	Sequence 2134, Ap
23	15.8	79.0	2009	10	US-09-764-869-2139	Sequence 2139, Ap
24	15.8	79.0	2378	10	US-09-815-242-4659	Sequence 4659, Ap
25	15.8	79.0	2595	10	US-09-954-456-211	Sequence 211, App
26	15.8	79.0	2595	10	US-09-954-456-503	Sequence 503, App
27	15.8	79.0	5950	10	US-09-880-107-3346	Sequence 3346, App
28	15.8	79.0	17993	10	US-09-768-781-5	Sequence 5, Appli
29	15.8	79.0	49136	10	US-09-768-877-1	Sequence 1, Appli
30	15.8	79.0	56516	9	US-09-853-526-1	Sequence 1, Appli
31	15.8	79.0	56516	10	US-09-901-484A-1	Sequence 1, Appli
32	15.8	79.0	56520	9	US-09-853-526-179	Sequence 179, App
33	15.8	79.0	56520	10	US-09-901-484A-179	Sequence 179, App
34	15.4	77.0	162	10	US-09-783-590-5917	Sequence 5917, App
35	15.4	77.0	267	10	US-09-878-574-9170	Sequence 9170, Ap
36	15.4	77.0	267	10	US-09-878-574-12010	Sequence 12010, A
37	15.4	77.0	268	10	US-09-878-574-11017	Sequence 11017, A
38	15.4	77.0	280	10	US-09-878-574-11701	Sequence 11701, A
39	15.4	77.0	346	9	US-09-954-531-103	Sequence 103, App
40	15.4	77.0	392	10	US-09-867-701-6405	Sequence 6405, Ap
41	15.4	77.0	416	10	US-09-880-107-3588	Sequence 3588, Ap
42	15.4	77.0	444	10	US-09-826-312-3	Sequence 3, Appli
43	15.4	77.0	447	9	US-09-938-842A-493	Sequence 493, App
44	15.4	77.0	636	10	US-09-770-149-641	Sequence 641, App
45	15.4	77.0	761	10	US-09-833-381-894	Sequence 894, App

ALIGNMENTS

RESULT 1
US-09-865-579A-14
Sequence 14, Application US/09865579A
Patent No. US20020098492A1
GENERAL INFORMATION:
APPLICANT: Taya, Yoshiaki
APPLICANT: Ishiguro, Takahiko
APPLICANT: Salto, Juichi
TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
FILE REFERENCE: 9558-003-27
CURRENT APPLICATION NUMBER: US/09/865, 579A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: JP 2000-163149
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-179394
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide capable of binding specifically to meca gene
US-09-865-579A-14
Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6, 5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 TCATTGCTGTAATATTTT 20
1 TCATTGCTGTAATATTTT 20
RESULT 2
US-09-865-579A-24
Sequence 24 Application US/09865579A
Patent No. US20020098492A1
GENERAL INFORMATION:

APPLICANT: Taya, Toshiki
APPLICANT: Ishiguro, Takahiko
TITLE OF INVENTION: Saito, Juichi
TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
FILE REFERENCE: 9558-003-27
CURRENT APPLICATION NUMBER: US/09/865,579A
CURRENT FILING DATE: 2001-05-28
PRIOR APPLICATION NUMBER: JP 2000-163149
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-179394
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-09-865-579A-24

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATTGCTGTTAATATTTT 20
Db 1 TCATTGCTGTTAATATTTT 20

RESULT 3
US-09-452-599-169/c
Sequence 169, Application US/09452599
Patent No. US20020055101A1
GENERAL INFORMATION:
APPLICANT: Bergeron, Michel G.
APPLICANT: Ouellette, Marc
TITLE OF INVENTION: Roy, Paul H.
TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
TITLE OF INVENTION: To Rapidly Detect and Identify Common Bacterial
TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
FILE REFERENCE: 12287.31
CURRENT APPLICATION NUMBER: US/09/452,599
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 08/526,840
PRIOR FILING DATE: 1995-09-11
PRIOR APPLICATION NUMBER: 08/304,732
PRIOR FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 177
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 169
LENGTH: 2007
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match 100.0%; Score 20; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATTGCTGTTAATATTTT 20
Db 1234 TCATTGCTGTTAATATTTT 1215

RESULT 4
US-10-001-843-114
Sequence 114, Application US/10001843
Patent No. US20020132255A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana

APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Calferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes an
FILE REFERENCE: DEX-0267
CURRENT APPLICATION NUMBER: US/10/001,843
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,992
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 218
SOFTWARE: PatentIn version 3.1
SEQ ID NO 114
LENGTH: 648
TYPE: DNA
ORGANISM: Homo sapien
US-10-001-843-114

Query Match 92.0%; Score 18.4; DB 12; Length 648;
Best Local Similarity 95.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCATTGCTGTTAATATTTT 20
Db 61 TAATTGCTGTTAATATTTT 80

RESULT 5
US-10-001-843-115
Sequence 115, Application US/10001843
Patent No. US20020132255A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Calferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes an
FILE REFERENCE: DEX-0267
CURRENT APPLICATION NUMBER: US/10/001,843
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,992
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 218
SOFTWARE: PatentIn version 3.1
SEQ ID NO 115
LENGTH: 928
TYPE: DNA
ORGANISM: Homo sapien
US-10-001-843-115

Query Match 92.0%; Score 18.4; DB 12; Length 928;
Best Local Similarity 95.0%; Pred. No. 40;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCATTGCTGTTAATATTTT 20
Db 341 TAATTGCTGTTAATATTTT 360

RESULT 6
US-09-764-864-1678
Sequence 1678, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864

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; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1678
; LENGTH: 32191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1678
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Query Match          84.0%; Score 16.8; DB 10; Length 32191;
Best Local Similarity 90.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 TCATTGCTTAATATTTT 20
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Db 8813 TAATTGTTGTTAATATTTT 8832
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RESULT 7
S-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: SATANABE, HIDEMI
; APPLICANT: MATSUKI, MASAHIRA
; APPLICANT: SAKAKI, YOSHITSUKI
; TITLE OF INVENTION: GENE/DNA OF BACTERIAL SYMPTOM OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
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Query Match          84.0%; Score 16.8; DB 10; Length 640681;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 TCATTGCTTAATATTTT 20
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Db 517674 TCATTGATTAATATTTT 517655
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RESULT 8
US-09-815-242-4716/c
; Sequence 4716, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
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; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4,716
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4716
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Query Match          80.0%; Score 16; DB 10; Length 963;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 4 TTGCTGTTAATATTTT 19
    ||||| ||||| ||||| |||||
Db 64 TTGCTGTTAATATTTT 49
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```
RESULT 9
US-09-815-242-8596/c
; Sequence 8596, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8596
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(966)
US-09-815-242-8596
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Query Match          80.0%; Score 16; DB 10; Length 966;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 4 TTGCTGTAATATTTT 19
|||||
Db 64 TTGCTGTAATATTTT 49

RESULT 10

US-09-815-242-8623/C
Sequence 8623, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8623
LENGTH: 966
TYPE: DNA
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(966)
US-09-815-242-8623

Query Match 80.0%; Score 16; DB 10; Length 966;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TTGCTGTAATATTTT 19
|||||
Db 64 TTGCTGTAATATTTT 49

RESULT 11

US-09-790-988-1
Sequence 1, Application US/09790988
Patent No. US20020127687A1
GENERAL INFORMATION:

APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEKI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS

FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 1
LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 80.0%; Score 16; DB 10; Length 640681;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATGCTGTAATAT 16
|||||
Db 306205 TCATGCTGTAATAT 306220

RESULT 12

US-09-783-590-6025/C
Sequence 6025, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:

APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 6025
LENGTH: 124
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (3)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (7)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (33)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (106)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (123)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-6025

Query Match 79.0%; Score 15.8; DB 10; Length 124;
Best Local Similarity 85.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TCATGCTGTAATATTTT 20
|||||
Db 38 TCATGCTGTAATATTTT 19

RESULT 13

US-09-983-965-4889

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; Sequence 4889, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 4889
; LENGTH: 187
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (114)
; OTHER INFORMATION:
; OTHER INFORMATION: Clone ID: 23-LIB34-073-Q1-E1-F3
US-09-983-965-4889

Query Match          79.0%; Score 15.8; DB 10; Length 187;
Best Local Similarity 89.5%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TCATTGCTGTAAATATTTT 19
        ||||| ||||| ||||| |||||
DB      72 TCATAGCTGTAAATATTTGT 90

RESULT 14
US-09-783-590-5750/c
; Sequence 5750, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5750
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (77)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (121)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (185)
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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (189)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-5750

Query Match          79.0%; Score 15.8; DB 10; Length 191;
Best Local Similarity 89.5%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TCATTGCTGTAAATATTTT 19
        ||||| ||||| ||||| |||||
DB      39 TCATTACTGTAAACATTTT 21

RESULT 15
US-09-983-965-4863
; Sequence 4863, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 4863
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION:
; OTHER INFORMATION: Clone ID: 22-LIB34-075-Q1-E1-F5
US-09-983-965-4863

Query Match          79.0%; Score 15.8; DB 10; Length 345;
Best Local Similarity 89.5%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TCATTGCTGTAAATATTTT 19
        ||||| ||||| ||||| |||||
DB      227 TCATTGCACTTAATATTTGT 245
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Search completed: December 11, 2002, 06:14:01
Job time : 259.922 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 : Search time 27.2626 Seconds
(without alignments)
224,980 Million cell updates/sec

Title: US-09-865-579a-24

Perfect score: 20

Sequence: 1 tcatgtcgttaataatttt 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
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4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	2007	2 US-08-743-637B-169	Sequence 169, App
C 2	20	100.0	2007	3 US-08-526-840B-169	Sequence 169, App
C 3	20	100.0	2028	4 US-09-134-001C-1710	Sequence 1710, App
4	13	90.0	27	2 US-08-743-637B-262	Sequence 262, App
5	17	85.0	330	2 US-08-437-013-4	Sequence 4, Appl
6	17	85.0	641	2 US-08-437-013-1	Sequence 1, Appl
7	17	85.0	641	2 US-08-437-013-28	Sequence 28, Appl
8	17	85.0	709	2 US-08-437-013-26	Sequence 26, Appl
9	16.8	84.0	805	1 US-08-118-169A-6	Sequence 6, Appl
10	16.8	84.0	2119	4 US-09-240-639-7	Sequence 7, Appl
11	16.8	84.0	11613	4 US-09-453-702B-42	Sequence 42, Appl
C 12	16.4	82.0	4326	2 US-08-852-807-12	Sequence 12, Appl
13	16	80.0	13674	2 US-08-852-807-1	Sequence 1, Appl
14	16	80.0	13674	3 US-09-071-606-11	Sequence 11, Appl
15	15.8	79.0	136	1 US-08-334-254-21	Sequence 21, Appl
C 16	15.8	79.0	136	2 US-08-334-254-28	Sequence 28, Appl
C 17	15.8	79.0	136	1 US-08-848-131-21	Sequence 21, Appl
C 18	15.8	79.0	136	2 US-08-848-131-28	Sequence 28, Appl
C 19	15.8	79.0	136	5 PCT-US95-14792-21	Sequence 21, Appl
C 20	15.8	79.0	136	5 PCT-US95-14792-28	Sequence 28, Appl
C 21	15.8	79.0	136	5 PCT-US95-14792-21	Sequence 21, Appl
C 22	15.8	79.0	831	4 US-09-134-001C-2270	Sequence 2270, App
C 23	15.8	79.0	1607	4 US-09-853-768-13	Sequence 13, Appl
C 24	15.8	79.0	1827	4 US-09-134-001C-1914	Sequence 1914, App
25	15.8	79.0	1929	2 US-08-892-770-2	Sequence 2, Appl
26	15.8	79.0	1971	2 US-08-892-770-4	Sequence 4, Appl
27	15.8	79.0	1981	4 US-09-647-590-17	Sequence 17, Appl

28	15.8	79.0	4129	2 US-08-370-319C-12	Sequence 12, Appl
29	15.8	79.0	4129	4 US-09-224-834-12	Sequence 12, Appl
30	15.8	79.0	6506	4 US-09-453-702B-1	Sequence 1, Appl
C 31	15.8	79.0	9064	4 US-08-961-527-17	Sequence 17, Appl
C 32	15.8	79.0	10207	1 US-08-920-812-2	Sequence 2, Appl
C 33	15.8	79.0	10207	1 US-08-920-827-2	Sequence 2, Appl
C 34	15.8	79.0	10207	1 US-08-921-177-2	Sequence 2, Appl
C 35	15.8	79.0	10207	1 US-08-362-577C-2	Sequence 2, Appl
C 36	15.8	79.0	10207	2 US-08-920-828-2	Sequence 2, Appl
37	15.8	79.0	49136	4 US-09-422-869-1	Sequence 1, Appl
38	15.8	79.0	56516	2 US-08-996-306-1	Sequence 1, Appl
39	15.8	79.0	56516	4 US-09-338-907-1	Sequence 1, Appl
40	15.8	79.0	56516	4 US-09-218-207-1	Sequence 1, Appl
41	15.8	79.0	56520	4 US-09-338-907-179	Sequence 179, App
42	15.8	79.0	56520	4 US-09-218-207-179	Sequence 179, App
43	15.8	79.0	162450	4 US-09-345-882-1	Sequence 1, Appl
C 44	15.4	77.0	78	1 US-08-351-748-19	Sequence 19, Appl
C 45	15.4	77.0	78	1 US-08-430-536A-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-743-637B-169/C
Sequence 169, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
NUMBER OF INVENTIONS: 273
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: O'ARLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5500
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0%; Score 20; DB 2; Length 2007;

Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
DB 1234 TCATTGCTGTTAATATTTT 1215

RESULT 2

US-08-526-840B-169/C
Sequence 169, Application US/08526840B
Patent No. 6001564

GENERAL INFORMATION:

APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: APPLICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/304,732

FILING DATE: 12-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: BAKER, Jean C.

REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET INFORMATION:

TELEPHONE: (414) 277-5000

TELEFAX: (414) 277-5591

INFORMATION FOR SEQ ID NO: 169:

SEQUENCE CHARACTERISTICS:

LENGTH: 2007 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-526-840B-169

Query Match 100.0%; Score 20; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
DB 1234 TCATTGCTGTTAATATTTT 1215

RESULT 3

US-09-134-001C-1710/C
Sequence 1710, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 1710

LENGTH: 2028

TYPE: DNA

ORGANISM: Staphylococcus epidermidis

FEATURE:

NAME/KEY: unsure

LOCATION: (52)

OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.

US-09-134-001C-1710
Query Match 100.0%; Score 20; DB 4; Length 2028;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
DB 1255 TCATTGCTGTTAATATTTT 1236

RESULT 4

US-08-743-637B-262
Sequence 262, Application US/08743637B

Patent No. 5994066

GENERAL INFORMATION:

APPLICANT: BERGERON, Michel G.

APPLICANT: PICARD, Francois J.

APPLICANT: OUELLETTE, Marc

APPLICANT: ROY, Paul H.

TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA

TITLE OF INVENTION: PROBES AND APPLICATION PRIMERS TO RAPIDLY DETECT AND

TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED

TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

ADDRESSEE: QUARLES & BRADY

STREET: 411 EAST WISCONSIN AVENUE

CITY: MILWAUKEE

STATE: WISCONSIN

COUNTRY: USA

ZIP: 53202-4497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/743,637B

FILING DATE: 04-NOV-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/526,840

FILING DATE: 11-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: BAKER, Jean C.

REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET INFORMATION:

TELEPHONE: (414) 277-5000

TELEFAX: (414) 277-5591

INFORMATION FOR SEQ ID NO: 262:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-743-637B-262

Query Match 90.0%; Score 18; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATTGCTGTTAATATTTT 20
|||||
DB 1 ATTGCTGTTAATATTTT 18

RESULT 5
US-08-437-013-4
Sequence 4; Application US/08437013
Patent No. 5932220
GENERAL INFORMATION:
APPLICANT: Barbours, Alan G.
APPLICANT: Carter, Carol
TITLE OF INVENTION: Diagnostic Tests for a New Spriochrome, Borrelia
TITLE OF INVENTION: lonestari sp. nov.
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,013
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSK:276/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-300
TELEFAX: 512/747-7577
TELEX: NA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"

US-08-437-013-4

Query Match 85.0%; Score 17; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATTGCTGTTAATATTTT 19
|||||
DB 116 ATTGCTGTTAATATTTT 132

RESULT 6
US-08-437-013-1
Sequence 1; Application US/08437013
Patent No. 5932220
GENERAL INFORMATION:
APPLICANT: Barbours, Alan G.
APPLICANT: Carter, Carol
TITLE OF INVENTION: Diagnostic Tests for a New Spriochrome, Borrelia

TITLE OF INVENTION: lonestari sp. nov.
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,013
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSK:276/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-300
TELEFAX: 512/747-7577
TELEX: NA
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 641 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"

US-08-437-013-1

Query Match 85.0%; Score 17; DB 2; Length 641;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATTGCTGTTAATATTTT 19
|||||
DB 253 ATTGCTGTTAATATTTT 269

RESULT 7
US-08-437-013-28
Sequence 28; Application US/08437013
Patent No. 5932220
GENERAL INFORMATION:
APPLICANT: Barbours, Alan G.
APPLICANT: Carter, Carol
TITLE OF INVENTION: Diagnostic Tests for a New Spriochrome, Borrelia
TITLE OF INVENTION: lonestari sp. nov.
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,013
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.

REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSK:276/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-300
TELEFAX: 512/747-7577
TELEX: NA
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 641 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-437-013-28

Query Match 85.0%; Score 17; DB 2; Length 641;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATTGCTGTTAATATTTT 19
|||||
JB 253 ATTGCTGTTAATATTTT 269

RESULT 8
US-08-437-013-26
Sequence 26, /pplication US/08437013
Patent No. 5932220
GENERAL INFORMATION:
APPLICANT: Barbour, Alan G.
TITLE OF INVENTION: Diagnostic Tests for a New Sprichete, Borrellia
TITLE OF INVENTION: Ionostari sp. nov.
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,013
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSK:276/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-300
TELEFAX: 512/747-7577
TELEX: NA
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-437-013-26

Query Match 85.0%; Score 17; DB 2; Length 709;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ATTGCTGTTAATATTTT 19
|||||
DB 292 ATTGCTGTTAATATTTT 308

RESULT 9
US-08-118-469A-6
Sequence 6, Application US/08118469A
Patent No. 5656451
GENERAL INFORMATION:
APPLICANT: Flavell, Richard A.
APPLICANT: Fikrig, Erol
APPLICANT: Lam, Tuan T.
APPLICANT: Kantor, Fred S.
APPLICANT: Barthold, Stephen W.
TITLE OF INVENTION: NOVEL B. BURGDOFFERI POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,469A
FILING DATE: 08-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,757
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: YU-102C1P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 805 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 130..711
US-08-118-469A-6

Query Match 84.0%; Score 16.8; DB 1; Length 805;
Best Local Similarity 90.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATGCTGTTAATATTTT 20
|||||
DB 163 TCATGCTGTTAATATTTT 182

RESULT 10
US-08-909-119-6
Sequence 6, Application US/08909119
Patent No. 5807685
GENERAL INFORMATION:
APPLICANT: Flavell, Richard A.
APPLICANT: Fikrig, Erol

```

: APPLICANT: Lam, Tuan T.
: APPLICANT: Kantor, Fred S.
: APPLICANT: Harthold, Stephen W.
: TITLE OF INVENTION: NOVEL B. BUKGDORFERI POLYPEPTIDES
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: c/o FISH & NEAVE
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10022
: COMPUTER READABLE FORM:
: MEDIUM TYPE: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/909,119
: FILING DATE: 11-AUG-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/118,469
: FILING DATE: 08-SEP-1993
: APPLICATION NUMBER: US 08/099,757
: FILING DATE: 30-JUL-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Haley Jr., James F.
: REGISTRATION NUMBER: 27,794
: REFERENCE/DOCKET NUMBER: YU-102CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 596-9000
: TELEFAX: (212) 596-9090
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 805 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 130..711
: US-08-909-119-6

Query Match      84.0%; Score 16.8; DB 1; Length 805;
Best Local Similarity 90.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATTCCTCTTAATATTTT 20
    |||||  |||||  |||||
Db 163 TCATTCCTCTTAATATTTT 182

RESULT 11
US-09-240-639-7
: Sequence 7, Application US/09240639
: Patent No. 6350447
: GENERAL INFORMATION:
: APPLICANT: Chadwick, Brian Paul
: APPLICANT: Frischaut, Anna-Maria
: TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
: TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
: FILE REFERENCE: 9598-066
: CURRENT APPLICATION NUMBER: US/09/240,639
: CURRENT FILING DATE: 1998-01-29
: NUMBER OF SEQ ID NOS: 29
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 7
: LENGTH: 2119
: TYPE: DNA
```

```

: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (205)..(1599)
: US-09-240-639-7

Query Match      84.0%; Score 16.8; DB 4; Length 2119;
Best Local Similarity 90.0%; Pred. No. 65;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATTCCTCTTAATATTTT 20
    |||||  |||||  |||||
Db 1933 TCATTCCTCTTAATATTTT 1952

RESULT 12
US-09-453-702B-42/C
: Sequence 42, Application US/09453702B
: Patent No. 6365723
: GENERAL INFORMATION:
: APPLICANT: Blatner, Frederick R.
: Burland, Valerie
: Perna, Nicole T.
: Plunkett, Guy
: Welch, Rod
: TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
: NUMBER OF SEQUENCES: 265
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Quarles & Brady
: STREET: 1 South Plinckney Street
: CITY: Madison
: STATE: WI
: COUNTRY: US
: ZIP: 53701-2113
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word Perfect 8.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/453,702B
: FILING DATE: 03-Dec-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/110,955
: FILING DATE: 04-Dec-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Seay, Nicholas J.
: REGISTRATION NUMBER: 27386
: REFERENCE/DOCKET NUMBER: 960296,95017
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (608) 251-5000
: TELEFAX: (608) 251-9166
: INFORMATION FOR SEQ ID NO: 42:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11613
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 42:
: US-09-453-702B-42

Query Match      82.0%; Score 16.4; DB 4; Length 11613;
Best Local Similarity 94.4%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATTCGTGTTAATATTTT 19
    |||||  |||||  |||||
Db 247 CATTCGTGTTAATATTTT 230

RESULT 13
```

```

US-08-852-807-12
; Sequence 12, Application US/08852807
; Patent No. 5861298
; GENERAL INFORMATION:
; APPLICANT: Debouck, Christine
; APPLICANT: Drake, Fred
; APPLICANT: Gowen, Maxine
; APPLICANT: Rood, Julie
; APPLICANT: Hastings, Gregg
; APPLICANT: Adams, Mark
; APPLICANT: Fraser, Claire
; APPLICANT: Lee, No. 5861298man
; APPLICANT: Kirkness, Ewen
; APPLICANT: Blake, Judith
; APPLICANT: Filzgerald, Lisa
; TITLE OF INVENTION: CATHEPSIN K GENE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,807
; FILING DATE: 07-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,942
; FILING DATE: 14-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/020,273
; FILING DATE: 17-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026,273
; FILING DATE: 26-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50006-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4326 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-852-807-12

```

```

Query Match      80.0%; Score 16; DB 2; Length 4326;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 3 ATTGCTGTATATTT 18
    |||||||
Db 3174 ATTGCTGTATATTT 3189

```

RESULT 14

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US-08-852-807-1
; Sequence 1, Application US/08852807
; Patent No. 5861298
; GENERAL INFORMATION:
; APPLICANT: Debouck, Christine
; APPLICANT: Drake, Fred
; APPLICANT: Gowen, Maxine
; APPLICANT: Rood, Julie
; APPLICANT: Hastings, Gregg
; APPLICANT: Adams, Mark
; APPLICANT: Fraser, Claire
; APPLICANT: Lee, No. 5861298man
; APPLICANT: Kirkness, Ewen
; APPLICANT: Blake, Judith
; APPLICANT: Filzgerald, Lisa
; TITLE OF INVENTION: CATHEPSIN K GENE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,807
; FILING DATE: 07-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,942
; FILING DATE: 14-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/020,273
; FILING DATE: 17-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026,273
; FILING DATE: 26-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50006-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-852-807-1

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```

Query Match      80.0%; Score 16; DB 2; Length 13674;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 3 ATTGCTGTATATTT 18
    |||||||
Db 8556 ATTGCTGTATATTT 8571

```

RESULT 15

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US-09-071-606-11
; Sequence 11, Application US/09071606
; Patent No. 6136365
; GENERAL INFORMATION:
; APPLICANT: Wertz et al.
; TITLE OF INVENTION: Attenuation of Negative Stranded
; TITLE OF INVENTION: RNA Viruses By Rearrangement of Their Genes and Uses Thereof
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,606
; FILING DATE: May 1, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5936
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 777-2321
; TELEFAX: (713) 777-6908
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 basepairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHEICAL: no
; ANTI-SENSE: no
;
US-09-071-606-11

```

```

Query Match          79.0%; Score 15.8; DB 3; Length 34;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CATGCTGTTAATATTTT 20
        |||||
Db      15 CATGCTGTTAGTTT 33

```

Search completed: December 10, 2002, 22:54:47
 Job time : 32.3876 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 ; Search time 433.631 Seconds

(without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579A-24

Perfect score: 20
Sequence: 1 tcatgtcgttaataatttt 20Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Genbankl :*

1: gb_da :*

2: gb_htg :*

3: gb_in :*

4: gb_om :*

5: gb_ov :*

6: gb_pat :*

7: gb_ph :*

8: gb_pl :*

9: gb_pr :*

10: gb_ro :*

11: gb_sts :*

12: gb_sy :*

13: gb_un :*

14: gb_vl :*

15: em_da :*

16: em_fun :*

17: em_hum :*

18: em_in :*

19: em_mu :*

20: em_om :*

21: em_of :*

22: em_ov :*

23: em_pat :*

24: em_ph :*

25: em_pl :*

26: em_ro :*

27: em_sts :*

28: em_un :*

29: em_vl :*

30: em_htg_hum :*

31: em_htg_inv :*

32: em_htg_other :*

33: em_htg_mus :*

34: em_htg_pln :*

35: em_htg_rod :*

36: em_htg_mam :*

37: em_htg_vrt :*

38: em_sy :*

39: em_htgo_hum :*

40: em_htgo_mus :*

41: em_htgo_other :*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6 AX306855	AX306855 Sequence
2	20	100.0	20	6 AX306865	AX306865 Sequence
3	20	100.0	467	6 A44526	A44526 Sequence 2
4	20	100.0	1789	6 E09772	E09772 The base se
5	20	100.0	2007	6 AR089410	AR089410 Sequence
6	20	100.0	2007	6 AR093610	AR093610 Sequence
7	20	100.0	2322	6 SARP	SARP
8	20	100.0	2322	6 E03736	E03736
9	20	100.0	2454	6 SEMECAPB	SEMECAPB
10	20	100.0	2455	6 E09771	E09771 The base se
11	20	100.0	2456	6 SAMECAPB	SAMECAPB
12	20	100.0	2456	6 AX110445	AX110445 Sequence
13	20	100.0	5596	1 SSR8MECA	SSR8MECA
14	20	100.0	6368	1 SSR3MECA2	SSR3MECA2
15	20	100.0	9047	1 SAMECAR11	SAMECAR11
16	20	100.0	21777	1 AB063173	AB063173 Staphyloc
17	20	100.0	26090	1 AB063172	AB063172 Staphyloc
18	20	100.0	39332	1 AB033763	AB033763 Staphyloc
19	20	100.0	58237	1 D86934	D86934 Staphylococ
20	20	100.0	68256	1 AB037671	AB037671 Staphyloc
21	20	100.0	290250	1 AP004822	AP004822 Staphyloc
22	20	100.0	298050	1 AP003129	AP003129 Staphyloc
23	20	100.0	349999	1 AP003358	AP003358 Staphyloc
24	19	95.0	150964	9 AC092374	AC092374 Homo sapi
25	19	95.0	201382	9 AC092721	AC092721 Homo sapi
26	18.4	92.0	159	11 G15937	G15937 human STS C
27	18.4	92.0	3720	9 S57132	S57132 COL16A1-tyr
28	18.4	92.0	5068	1 SSR1MECA	SSR1MECA
29	18.4	92.0	5387	9 HUMCOL16A	HUMCOL16A
30	18.4	92.0	5387	11 G28574	G28574 human STS S
31	18.4	92.0	6684	1 SSR1MECA	SSR1MECA
32	18.4	92.0	10520	1 AE013857	AE013857 Yersinia
33	18.4	92.0	68398	2 AC131045	AC131045 Homo sapi
34	18.4	92.0	73141	2 AC025123	AC025123 Homo sapi
35	18.4	92.0	97194	2 AC127723	AC127723 Rattus no
36	18.4	92.0	97786	2 AC111926	AC111926 Rattus no
37	18.4	92.0	97968	2 AF003530	AF003530 Homo sapi
38	18.4	92.0	111290	2 AC115462	AC115462 Rattus no
39	18.4	92.0	115184	2 AC127170	AC127170 Medicago
40	18.4	92.0	129677	2 AC127035	AC127035 Homo sapi
41	18.4	92.0	135631	9 AL512649	AL512649 Human DNA
42	18.4	92.0	141386	2 AC119454	AC119454 Rattus no
43	18.4	92.0	143813	9 AC002994	AC002994 Homo sapi
44	18.4	92.0	143909	9 AC104454	AC104454 Homo sapi
45	18.4	92.0	148661	2 AC126738	AC126738 Rattus no

ALIGNMENTS

RESULT 1
AX306855
LOCUS Sequence 14 from Patent EP1160333. 20 bp. DNA linear PAT 14-DEC-2001
DEFINITION AX306855
ACCESSION AX306855
VERSION AX306855.1 GI:17894677
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 Taya, T., Ishiguro, T. and Salto, J.
AUTHORS
Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
TITLE
JOURNAL Patent: EP 1160333-A 14 05-DEC-2001;

FEATURES Tosoh Corporation (JP)
Source Location/Qualifiers
1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide capable of binding specifically to meca gene or RNA derived from said gene"

BASE COUNT 4 a 2 c 2 g 12 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATTGCTGTTAATATTTT 20
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1 TCATTGCTGTTAATATTTT 20

DB 1 TCATTGCTGTTAATATTTT 20

RESULT 2
X306865
ACUS AX306865 20 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 24 from Patent EP1160333.
ACCESSION AX306865
VERSION AX306865.1 GI:17894687
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.

REFERENCE 1
AUTHORS Taya,T., Ishiguro,T. and Saito,J.
TITLE Oligonucleotides and method for detection of meca gene of methicillin-resistant Staphylococcus aureus
JOURNAL Patent: EP 1160333-A 24 05-DEC-2001;
Tosoh Corporation (JP)
Location/Qualifiers

FEATURES
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 4 a 2 c 2 g 12 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATTGCTGTTAATATTTT 20
|||||
1 TCATTGCTGTTAATATTTT 20

RESULT 3
A44526
LOCUS A44526 467 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 2 from Patent WO9513395.
ACCESSION A44526
VERSION A44526.1 GI:2299344
KEYWORDS
SOURCE
ORGANISM
Staphylococcus aureus.
Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1 (bases 1 to 467)
AUTHORS Springer,W. and Endermann,R.
TITLE SPECIFIC GENE PROBES AND METHODS FOR QUANTITATIVE DETECTION OF METHICILLIN-RESISTANT STAPHYLOCOCCI
JOURNAL Patent: WO 9513395-A 2 18-MAR-1995;
BAYER AG (DE)
Other publication DE 4338119 950511.
Location/Qualifiers

COMMENT 1..467
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"

BASE COUNT 187 a 73 c 85 g 122 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 467;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATTGCTGTTAATATTTT 20
|||||
210 TCATTGCTGTTAATATTTT 191

DB 210 TCATTGCTGTTAATATTTT 191

RESULT 4
E09772
LOCUS E09772 1789 bp RNA linear PAT 29-SEP-1997
DEFINITION The base sequence of modified meca DNA.
ACCESSION E09772
VERSION E09772.1 GI:22026401
KEYWORDS
SOURCE
ORGANISM
Staphylococcus aureus.
Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1 (bases 1 to 1789)
AUTHORS Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
TITLE NOVEL "MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL Patent: JP 1995209294-A 2 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/2
PD 11-AUG-1995
PP 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI MASAHISA,
PI SUGURO KAZUYA
PC GO1N3/53,C07K14/21,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC C12P19/19)
CC (C12P21/02,C12P1:19);
CC Strandedness: Double;
CC Topology: Linear;
FH Key
FH source 1..1789
FT 1..1608 /organism="Staphylococcus aureus" FT CNS
FT 1..1789 /product="Modified meca".
Location/Qualifiers

FEATURES
source 1..1789
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"

BASE COUNT 735 a 263 c 302 g 489 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1789;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATTGCTGTTAATATTTT 20
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835 TCATTGCTGTTAATATTTT 816

DB 835 TCATTGCTGTTAATATTTT 816

RESULT 5
AR089410/c
LOCUS AR089410 2007 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 169 from patent US 5994066.
ACCESSION AR089410
VERSION AR089410.1 GI:10016167
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2007)

AUTHORS Bergeron, M.G., Picard, F.J., Ouellette, M., and Roy, P.H.
 TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
 JOURNAL Patent: US 5994066-A 169 30-NOV-1999;
 FEATURES location/Qualifiers
 SOURCE 1. 2007
 BASE COUNT 855 a 270 c 341 g 541 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
 DB 1234 TCATTGCTGTTAATATTTT 1215

RESULT 6
 LOCUS AR093610/c AR093610 2007 bp DNA linear PAT 08-SEP-2000
 DEFINITION Sequence 169 from patent US 6001564.
 ACCESSION AR093610
 VERSION AR093610.1 GI:10020359
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2007)
 AUTHORS Bergeron, M.G., Ouellette, M., and Roy, P.H.
 TITLE Species specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
 JOURNAL Patent: US 6001564-A 169 14-DEC-1999;
 FEATURES location/Qualifiers
 SOURCE 1. 2007
 BASE COUNT 855 a 270 c 341 g 541 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 TCATTGCTGTTAATATTTT 20
 DB 1234 TCATTGCTGTTAATATTTT 1215

RESULT 7
 LOCUS SABB/c 2322 bp DNA linear RCT 12-SEP-1993
 DEFINITION Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible penicillin-binding protein.
 ACCESSION Y00688.1 GI:46628
 VERSION Y00688.1
 KEYWORDS penicillin-binding protein.
 SOURCE Staphylococcus aureus.
 ORGANISM Staphylococcus aureus
 Bacteria; Firmicutes; Bacillales; Staphylococcus.
 REFERENCE 1 (bases 1 to 2322)
 AUTHORS Song, M.D., Machi, M., Doi, M., Ishino, F., and Matsubashi, M.
 TITLE Evolution of an inducible penicillin-target protein in methicillin-resistant Staphylococcus aureus by gene fusion
 JOURNAL FEBS Lett. 221 (1), 167-171 (1987)
 MEDLINE 87304805
 PUBMED 3305073
 REFERENCE 2 (bases 1 to 2322)
 AUTHORS Kyte, J.C., Tesch, W., Birch-Machin, I., Reynolds, P.E.,

TITLE Barberis-Maino, L., Kayser, F.H., and Berger-Bachi, B.
 JOURNAL Sequence comparison of mecA genes isolated from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis
 MEDLINE 91033056
 PUBMED 2227446
 COMMENT Data kindly reviewed (13.1.88) by Matsubashi.
 FEATURES location/Qualifiers
 SOURCE 1. 2322
 ORGANISM="Staphylococcus aureus"
 /db_xref="taxon:1280"
 1. 2013
 /note="penicillin-binding protein (AA 1-670)"
 /codon_start=1
 /transl_table=11
 /protein_id="CAA68684.1"
 /db_xref="GI:46629"
 /db_xref="SWISS-PROT:P07944"
 /translation="MKKIKIPLILIVVVGFCIYVASKDK:INNTIDAIEDKFKQVYKDSYISKSDNGEVEETPERIKIYNSIGVGIQIDRKIKKSKKKRVADQYKIKTNGINIDRNVOGFNFKEDGMKRLMDHSVILPGMKDSIHIEELKSEBKKIDRNVELATGTGTHMRIGIYPRVSKKDYKAIKELISIEDYINNNKIKIGIKMISFHKYTKKMDRFLSDPAKRFHITNETSRNYPUGKATSHLGVGPINSEFLKQEKGYKDAVIGKKGLEKLYDKRLQHDQYKVFIVADQNSNTHATLIKKKKDKDQIQITDAKVOKSIYNNMKNDYGSCTAIHQICELALVSPSYDVYFPMQMSNEYNNKLTEDKEPLINKFOITTSFGSTOKILTAMIGLNKTLDDKTSYKIDGKMGOKSMGCVNTRYEVVNGNIDKQAIKESSDNIEFARVALLEGSKREKMKKLGVEDIPSPYPNQISNKLNDNEIILADSGVGCGELLINPVQILSYSLKNGNINAPHILKDKNNVYMKNIISK KENTINLNDGQGVNKTTHKEDTIRSYANLIGKSGTALMKKQCTGRQIQWPISTYK DNPMMATINVDVODKGMASYNKISCKYVDELYENKRYDIDE"

BASE COUNT 940 a 324 c 389 g 669 t
 ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 2322;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
 DB 1240 TCATTGCTGTTAATATTTT 1221

RESULT 8
 LOCUS E03736/c 2322 bp DNA linear PAT 29-SEP-1997
 DEFINITION DNA sequence of PBP2' gene for determination of methicillin resistance.
 ACCESSION E03736
 VERSION E03736.1 GI:2171951
 KEYWORDS JP 1992169200-A/9.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 2322)
 AUTHORS Watanabe, Y., Nakamura, E., Teraoka, H., Wada, K., Minamide, W., and Murakami, K.
 TITLE DETECTION OF PBP 2' GENE AND JUDGEMENT OF METHICILLIN RESISTANCE
 JOURNAL Patent: JP 1992169200-A 9 17-JUN-1992;
 SHIONOGI & CO LTD
 OS (methicillin resistant)staphylococcus aureus
 PN JP 1992169200-A/9
 PD 17-JUN-1992
 PF 31-OCT-1990 JP 199026708
 PI WATANABE YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI, MINAMIDE WAKIO, MURAKAMI KAZUHISA
 PC C12Q1/68, C12N15/11;
 CC C strandy:ness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH key location/Qualifiers

FT misc_feature 1..2322
FT FT /note="PBP2' gene for determination of FT
methicillin resistance".
FEATURES
source 1..2322
/organism="unidentified"
/db_xref="taxon:32644"
HASH COUNT 939 a 324 c 390 g 669 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2322;
Best local similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
Db 1240 TCATTGCTGTTAATATTTT 1221

RESULT 9
LOCUS SMCAPB 2454 bp DNA linear BCF 12-SEP-1993
DEFINITION S.epidermidis meca gene for PBP2' (penicillin binding protein 2').
ACCESSION X52592.1 GI:46993
VERSION X52592.1 GI:46993
KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
penicillin-binding protein 2'.
SOURCE Staphylococcus epidermidis.
ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 2448)
AUTHORS Ryffel,C.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE 2 (bases 1 to 2454)
AUTHORS Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,
Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.
TITLE Sequence comparison of meca genes from methicillin-resistant
Staphylococcus aureus and Staphylococcus epidermidis
Gene (1990) in press
JOURNAL 3 (bases 1 to 2454)
AUTHORS Ryffel,C.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1990) Ryffel C., University of Zuerich, Inst of
Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE 4 (bases 1 to 2454)
AUTHORS Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,
Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.
TITLE Sequence comparison of meca genes isolated from
methicillin-resistant Staphylococcus aureus and Staphylococcus
epidermidis
Gene 94 (1), 137-138 (1990)
JOURNAL
MEDLINE 9103056
PUBMED 2227446
COMMENT See also <X52593-4> and <Y00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.
FEATURES
source 1..2454
/organism="Staphylococcus epidermidis"
/strain="WT55"
/db_xref="taxon:1282"
/clone="MT80/MT79"
80..85
/note="35 region"
101..105
/note="10 region"
130..134
/note="ribosome binding site"
141..2159
/note="primary transcript"
141..2147
CDS

/note="PBP2' (AA 1 - 668)"
/codon_start=1
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/db_xref="GI:46994"
/db_xref="SPTREMBL:Q54113"
/translation="MKKIVPLIVLVVVGFIYFVASKDEINNTIDALIEDKNEKQ
YKDSYISKSDGVEEMTERPIKIVNSGYVDINODRKIKVSKKKRVDQVYKIK
TNYCNIDRWVQFNVEYKDGMMKLDMDSYIIPGMOKDOSIHIENIKSHCKIIDHNNV
ELANTGTAEICIVPKNSKRDYKAIKALSLISHDYTKQMOMNVDPTFVPLATYV
KMDENYISDFAKRHILTNTEESRNPVLRKATSHIIGYVPIINSEIKQREYKQKDDA
VIGKRGLELYDKKLQHEDEGYRVTVVDNSNTIARTLIEKKRKDEKDIQITDAVYVK
SYNNMKNDYSGSTAIHPQTGELLAVSPDYVPFMYGMSNEEYKNTLEDKKEPL
NKFQITSPGSTOKITLTMIGLNNKTLDDKTSYKIDGKMGOKDSMGVNTVRYEVN
GNIDLKQALESSDNIPFARVALERLGSKREKMGKKLGVGEIDIPSDYPRYNAOISMKNI
DNEILLADSGGOGELLINPVQIISTVSLFENNCGINAPHLIKDKKVMYKKNISKE
NINLLTDGMQVYNNKTHKEDIYRSYANLIGKSGTALAKKQGTQRQIQWPISTYKDN
PNNMMAINVKDVOVDKGMASYNMAKISGYVDIYENGNKKYDIDE"
441..448
/note="altaaac was ac in [1]"
/citation=11
old_sequence 641..643
/note="agc was ac in [1]"
/citation=11
old_sequence 652..653
/note="ta was tta in [1]"
/citation=11
old_sequence 731..733
/note="caa was ca in [1]"
/citation=11
old_sequence 780..781
/note="ct was ctt in [1]"
/citation=11
BASE COUNT 997 a 345 c 398 g 714 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 2454;
Best local similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
Db 1374 TCATTGCTGTTAATATTTT 1355

RESULT 10
LOCUS E09771/C 2455 bp RNA linear PAT 29-SEP-1997
DEFINITION The base sequence of meca DNA.
ACCESSION E09771
VERSION E09771.1 GI:22026400
KEYWORDS JP 1995209294-A/1.
SOURCE Staphylococcus aureus.
ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 2455)
AUTHORS Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
TITLE NOVEL 'MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
Patent: JP 1995209294-A 1 11-AUG-1995;
JOURNAL KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/1
PD 11-AUG-1995
PF 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
MASAHISA,
PI SUGURO KAZUYA
PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,(C12N1/21, PC
C12R1:19),
PC (C12P21/02,C12R1:19);
CC strandedness: Double;
CC topology: Linear;

TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences X53818, X54660, L14020, X52593, Y09223.
FEATURES
source
1..5596
/organism="Staphylococcus sciuri"
/strain="K8 (ATCC700063)"
/sub_species="rodentius"
/db_xref="taxon:1296"
1..236
/gene="NTORF78"
/gene="NTORF78"
/codon_start=3
/transl_table=11
/protein_id="CAA73540.1"
/db_xref="GI:2791920"
/db_xref="SPTREMBL:054284"
/translation="AFRLKPDCHCTSTYNNLLIEDHRIHKVTKRQSYNTAKNTLK
GIFCIYALKKNNRSLOITGFSPCHEISIMLAS"
complement(485..856)
/gene="mecI"
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complement(485..856)
/codon_start=1
/transl_table=11
/product="MecI protein"
/protein_id="CAA73545.1"
/db_xref="GI:2791921"
/db_xref="SPTREMBL:054285"
/translation="MDNKTYEISSAEWEVNNI..MKRYASANYIEETOMOKDSPKT
IRFLIRLYKKGFIDRKDNKIKQYSLVESDQIKYTKSNFINKVYKGGNSLVNLF
VERKDIODEIEERNLNKK"
complement(join(856..2613,2620..2626,2638..2643))
gene
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complement(856..2613)
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/transl_table=1
/product="MecR1 protein"
/protein_id="CAA73546.1"
/db_xref="GI:2791922"
/translation="MLSSFLMLSIISLLTTCVILVRLVLYKYTONIMSHKWLVL
VSTLPIPLIPYKISNPFPSKDMNRNVSDFSSVSHMLDGOSSVTDLAINVQFET
SNITVYMLIMVFGSLCLPYMIKAPROIVIKSSLESSYLNERLKYCOSKMOFYK
HITISYSNIDNPVFGLVKSQIVLPVVEVTMDKELEYILHLSHVSKDILFNO
LYVEFKMIFNPALYTSKTMDCCKVCDRNLKTLNREHTRGSESLKGLS
QHINNAOYLILGFNSNIKERVKITAIYDSKPRNRKRIYATVCSISLILQPLLS
AHVOODKYEETNVSTKRLNQLAPYFKGFGDSVFLNEREQATSYNEPESKQRYSPNT
YKJYLAIMAPDQNLISLNHTEQOMDKHQYPRKEVNOONI.NSSMKYSVNMYMLNH
LRDEKSVYDLIHYGNEELISGENENWNEESLKLISALDOVNI.LKNMQUHMHFNNKA
IKVENSMTLKODPYKYVGKTCGCIYVNHKANGVGVYVEVKDNTYVFATHLKCEDNA
NGEKAQOISERILKEMELI"
complement(865..869)
gene
/gene="mec"
complement(865..869)
RBS
/gene="mecI"
complement(2620..2626)
/gene="mecR1"
complement(2638..2643)
-10_signal
/gene="mecR1"
2652..2657
/gene="meca"
2652..2657
-35_signal
/gene="meca"
complement(2663..2668)
/gene="mecR1"
complement(2663..2668)
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/gene="mecR1"
2676..4719
/gene="meca"
2676..2681
-10_signal

RBS
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2702..2707
/gene="meca"
2713..4719
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/protein_id="CAA73547.1"
/db_xref="GI:2791923"
/db_xref="SPTREMBL:054286"
/translation="MKKIKVPIPLIIVVVGFIYFASKKEINNTIDAIEDKNEKO
VYKDSYSIKSDNGEVEMTERRPIKIVVSLVGDQINODRKIKVSKKKKVDQYKIK
TNGCIDNRNVQPNFVKEDGMMKLDMDISVYIIPGMOQOSIHENLSEKRIIDRNV
ELANTGAYEIGTVPRKNSKDKAIKELISIEDYIKOOMDQWODTFVPLKTYK
KMDYELSDFAKKPHLTTNETESRNPYLEKATSHLGVGPINSHELKQLEYKQKIDA
VICKKGLELYDKKLQHEIDYRVYIYDONSNTIAHTLEKKKDKGNDIOLTDAAVOK
SIYNNMKNDGSGTAIHPOTGELLATVSTPSDYVPPMYGMSNEEYKLTEDKKEPLL
NKREITTSPSGSTOKILFAMIGLNKKTLDKTSYKIDGKGQKDSMGVQVTVREYVN
GNIDLKQATSSSDNIFPARVALDELGSKKFEKMKKILGVGDIPSDYVFFYAOISNNKL
DNEILADSCGCGEELINPYQLISYSALENNGNINAPHLKDTKRYKKNIIISKE
NINLTGMOQVNNKTHKEDIYRSYAWLICKSGTAEILMKQCEGTGOTGWFISTDKDN
PNMMAINVDVODKMAVYNAKISGVYDELVENCKKXYDIE"
complement(4765..5266)
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complement(4765..5193)
/gene="ORF142"
/codon_start=1
/transl_table=11
/protein_id="CAA73548.1"
/db_xref="GI:2791924"
/db_xref="SPTREMBL:054520"
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/gene="NTORF101"
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BASE COUNT 1991 a 856 c 821 g 1928 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 5596;
Best local Similarity 100.0%; Pred. No. 2,3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCATGCTGTTAAATATTTT 20
DB 3946 TCATTGCTGTATATATTTT 3927
RESULT 14
SSK3MECA2/c SSK3MECA2 6368 bp DNA linear BCT 16-JAN-1998
LOCUS S_sciuri_mecA2 gene, strain K3 (MM2).
DEFINITION Y13095
ACCESSION Y13095
VERSION Y13095.1 GI:2791912
KEYWORDS CTORF261 gene; mecA2 gene; mecI gene; mecR1 gene; NTORF101; ORF142.
SOURCE Staphylococcus sciuri.
ORGANISM Staphylococcus sciuri

REFERENCE 1 Bacteria: Firmicutes; Bacillales; Staphylococcus.
AUTHORS Wu, S., de Lencastre, H. and Tomasz, A.
TITLE Genetic organization of the mecA region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus sciuri
JOURNAL J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE 96101461
PubMed 9440511
REFERENCE 2 (bases 1 to 6368)
AUTHORS Wu, S.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences U14020, X52593, Y09223.
FEATURES
source Location/Qualifiers
1..6368
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/strain="K3 (M2)"
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SNITMILLVWFGSLCLFYMTAKFQIVDINSSLESSLYLNERLKVCOCKMOFYFK
HRTISYSSNIDNPMVFGVLQIPLPVAIVETMNDKEIYIILHELSHVSHDLIFNQ
LYVFKMIEMFNALYISKTMNDCEKVCDDRYLKLINRHEIRYGESTILCKPILS
OHINVAAGIYLGFNISNIKEKRYIALYDMPKPNRKRIVAYIVCSISILIOAPILS
AHVQODKYEITNVSYKKNLQALPYFKGDSFVLVNEPQAYSYINPESQORSPTS
KYIYALIMAFDNLISNHTEOODKHQYFPKENDQONLSSSKKSVNNTYELNKH
LRQDEKSTIDLIEYGNELISGNETSNWESSLSIALEOVNLLKDMQHNNHFDNKA
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TYNGNIDRNVOFNVEYKEDGMKLPMDHSV I IPGQKQDS I I FNLKSRGK I LIRNRY
ELANTGTAYEIGIYVKNYSKKDYKA I AKELISEDY I KOQMDMMVOODTFFPKTYV
KMEYLSDFAKKPHLTNETESRNPLEKATSHLGYGPIINSEIQLKQEKYKQKDA
VIGKKGLEKLYDKKLQHEQGYRYIVVDNSNTIAHTLEKKRKGKDIQLTIDAKYOK
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NKFOITTSYPSGTOK I LYAMIGLNKTLDDKTSYKIDGGMQKDSMGQVNTREVN
DNIDLKQA I EESSDNI I FARVALIELGSKKFEKGMKLAGHD I PSIDYFYNAQ I SKNL
DNELLADSGYGCCE I LINPOULISYSALENNGNINAPHLIKDTKNKVMKNN I ISKE
NINLTQMOQVYKTKEDIYRSYANLIGSGTAELMKOGETGRPIGW I ISYDKDN
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BASE COUNT 2230 a 998 c 884 g 2256 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 6368;
Best Local Similarity 100.0%; Pred. No. 2,2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATGCTGTTAATATTTT 20
|||||
Db 4718 TCATGCTGTTAATATTTT 4699

RESULT 15
SAMECAR1/C
LOCUS Staphylococcus aureus meca, mecl1, mecl genes and ORF168, ORF142,
DEFINITION ORF4, ORF145 and ORF224.
ACCESSION Y14051.1 GI:2791983
VERSION Y14051
KEYWORDS meca gene; mecl1 gene; mecl2 gene; ORF142; ORF145; ORF224; ORF44;
PBP2A; repressor protein; transposase.
ORGANISM Staphylococcus aureus.
JUNCF Staphylococcus aureus
REFERENCE 1 (bases 1 to 9047)
AUTHORS Wu, S.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-1997) S. Wu, Laboratory of Microbiology, The
Rockefeller University, 1230 York Avenue, New York, NY 10021, USA
REFERENCE 2 (bases 1 to 9047)
AUTHORS Wu, S., de Lencastre, H. and Tomasz, A.
TITLE Genetic organization of the meca region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus sciuri
JOURNAL J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE 98101461
PUBMED 9440511

FEATURES
source Location/Qualifiers
1..9047
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/db_xref="taxon:1280"
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/protein_id="CAA74375.1"
/db_xref="GI:2791991"

gene
CDS

/db_xref="GI:2791986"
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VSTLPIIPFYKISNFTSKDMKNNKRVSTISSVHMLDGOOSVTKDIAIVNOPT
SNITVIMLILWFGSLCLPYMKAFROIDVIKSSILESSYINELKACQSMQYKK
HITISYSSNIDNPNVFGIAVKSQIVIPVAVFPMNKLEIYIILHLEIYHKKSHDILFNO
LYVEKMIIFMNPALYISKTMDNDCEKCDNNYLILRNIEHIEYGESILKSLILKS
OHINNYAAOYILGFNSNIKERVYIALYOSMKPPNNKIVAYICYSISLQVALLS
AHVODKYETNYSYKKNLQALYFKGQSFVLYNREGASIVNEPESKOPSPNST
YKIYIALMAFDONLILNHTDOOMKHQTPKRNQODONLASSMAYSNMITEINI
LKHDEKYSTLDLLEYGNEFISGENENYNESSILKISAIFQVNIILKMKOHNMHIDKAI
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ELANTGTHRLGIVPNVSKDYKAIKELISSEYINNKWIKIGYKMIKPSHFETK
KMDYLSDPFAKKFHLITNTEFSRNPVLEAKTSHLIGYVCPINSEILKQREKYGKIDVA
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SIVNMKNNDYSGCTAIHPTGELLALVSPSYDVPYHMGKSNERYNKITDKRPPL
NKFOTTSFGSTOKITLNTATGLNNKTLDKITSYKIDGKQMDKSMGYNVTRFVFN
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/transl_table=11
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/protein_id="CAA74378.1"
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/db_xref="SPTREMBL:Q54083"
/translation="MYKEAGYELNVTYVTKPARANQLANMGVDGIFTDNADKRVHLSQ
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complement(6354..6791)
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/transl_table=11
/product="hypothetical protein"
/protein_id="CAA74379.1"
/db_xref="GI:2791990"
/db_xref="SPTREMBL:Q99387"
/translation="MLTYVGHGGLPSKAPERTIASPKAASEVGIINMIEIDVALTKDE
QULIILHDDILERTNMSGEITELANTDEIKDASAGWPFGEKPKDELPLPFDDVAKIANE
YMMNLNVELKGTGTGNGLALSKSMVKOYEEDLTJLNQOBEELI"
8096..8770
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gene
CDS

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SIMLAS"

BASE COUNT 3099 a 1469 c 1257 g 3222 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; length 9047;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
DB 4705 TCATTGCTGTTAATATTTT 4686

Search completed: December 10, 2002, 20:17:07
Job time : 437.756 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 ; Search time 1025.47 Seconds
(without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579A-24

Perfect score: 20
Sequence: 1 tcaatgcgttaataatttt 20

Scoring table:
IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

>al number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthu:*
3: em_estin:*
4: em_estlu:*
5: em_estlov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est12:*
11: gb_hic:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vtl:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	95.0	436	17	A0063885 HS_2186_B
C 2	18.4	92.0	205	14	BM874740 1aa07h11
C 3	18.4	92.0	274	9	AA770215 ab72h12.s
C 4	18.4	92.0	283	9	AA821323 vs67d07.r
C 5	18.4	92.0	289	12	BF223892 7g3ba07.x
C 6	18.4	92.0	298	9	A1656575 tt51h06.x

C 7	18.4	92.0	332	9	A1565925 tr94h12.x
C 8	18.4	92.0	336	9	AA682251 ab52d11.s
C 9	18.4	92.0	337	10	AW192414 X183c10.x
C 10	18.4	92.0	339	9	AA620929 a196d02.s
C 11	18.4	92.0	345	9	A1644998 vs67d07.y
C 12	18.4	92.0	352	10	AW594048 h944d02.x
C 13	18.4	92.0	356	9	AA678445 ah01c08.s
C 14	18.4	92.0	382	9	A1679677 t65c09.x
C 15	18.4	92.0	383	14	T29062 EST67294 flu
C 16	18.4	92.0	390	9	A1645664 vs67d07.x
C 17	18.4	92.0	390	9	A1582517 w043q08.x
C 18	18.4	92.0	395	9	A1582517 ts01h09.x
C 19	18.4	92.0	395	9	AU088039 AU088039
C 20	18.4	92.0	402	9	AA791476 vs66f07.r
C 21	18.4	92.0	405	9	A169276 w043q08.x
C 22	18.4	92.0	406	9	AA330228 EST33974
C 23	18.4	92.0	411	9	A1686616 LX08h12.x
C 24	18.4	92.0	437	9	A1783833 LU79f01.x
C 25	18.4	92.0	456	14	W95831 zc09c10.r1
C 26	18.4	92.0	456	14	W96115 zc09c10.s1
C 27	18.4	92.0	463	12	BF058423 7X30f11.x
C 28	18.4	92.0	479	9	AA662133 O148C02.s
C 29	18.4	92.0	485	9	A1589349 qf35a11.x
C 30	18.4	92.0	486	9	A1206895 qf35a11.x
C 31	18.4	92.0	488	9	AA088202 zK71c02.s
C 32	18.4	92.0	488	9	AA088202 zK71c02.s
C 33	18.4	92.0	489	9	A1089082 ou66h10.s
C 34	18.4	92.0	494	9	A1624537 ts30a08.x
C 35	18.4	92.0	494	10	AW950459 EST362529
C 36	18.4	92.0	502	10	A1131021 qB82e12.x
C 37	18.4	92.0	502	10	BE645315 7e60c05.x
C 38	18.4	92.0	518	12	BF063391 7h89c02.x
C 39	18.4	92.0	521	17	BH185493 027.L_23-
C 40	18.4	92.0	521	17	BH185493 027.L_23-
C 41	18.4	92.0	531	10	BE049264 xw98g05.x
C 42	18.4	92.0	549	14	BM672887 U1-R-C00-
C 43	18.4	92.0	558	9	A1801156 t085h11.x
C 44	18.4	92.0	558	12	Hf434543 707b04.x
C 45	18.4	92.0	569	13	BM314325 t953a12.x

ALIGNMENTS

RESULT 1
A0063885/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 436)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2186 row: N column: 1

Class: BAC ends
High quality sequence stop: 436.

FEATURES
Source
Location/Qualifiers
1..436
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT
147 a 87 c 62 g 133 t 7 others

ORIGIN
Query Match 95.0%; Score 19; DB 17; Length 436;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 19
|||||
198 TCATTGCTGTTAATATTTT 180

RESULT 2
BM874740 205 bp mRNA linear EST 07-MAR-2002
LOCUS la07h11.y1 8 5 week embryo anterior tongue 8 5 EAT Homo sapiens
DEFINITION cDNA 5', mRNA sequence.
ACCESSION BM874740
VERSION BM874740.1 GI:19242406
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 205)
Tidwell,R., Clifton,S., Marra,M., Hillier,L., Page,D., Martin,J.,
Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ralter,E., Bennet,J.,
Ronko,I., Tsagarisshvili,R., Belaygorod,L., Grow,A., Maguire,L.,
Waterston,R. and Wilson,R.
Washu Stem cell EST Project
Unpublished (2002)
TITLE JOURNAL
COMMENT Contact: Rose Tidwell
Washu Stem cell EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: eselw@wustl.edu
Tissue provided by Rose Tidwell Library was constructed by Yulia
and Rose Tidwell Library re-arrayed by Rose Tidwell DNA sequencing
by: Washington University Genome Sequencing Center For information
on obtaining a clone please contact: Rose Tidwell
(rtidwell@genetics.wustl.edu)
putative full length read
vector to vector length is 206
Seq primer: -40RP from Glibco.
Location/Qualifiers
1..205
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="8 5 week embryo anterior tongue 8 5 EAT"
/dev_stage="8.5 week embryo"
/lab_host="DH10B"
/note="Vector: pAMP1; Site: 1: no restr sites used in
cloning; Site: 2: no restr sites used in cloning; UDG
cloning; oligo dt primed 1st strand cDNA library"

BASE COUNT
82 a 23 c 37 g 62 t 1 others

ORIGIN
Query Match 92.0%; Score 18.4; DB 14; Length 205;
Best Local Similarity 95.0%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
Db 129 TAATTGCTGTTAATATTTT 148

RESULT 3
AA770215/c 274 bp mRNA linear EST 29-DEC-1998
LOCUS ah72h12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321223 3,
DEFINITION similar to SW:CAIF_HUMAN Q07092 COLLAGEN ALPHA 1(XVI) CHAIN
PRECURSOR.; mRNA sequence.
ACCESSION AA770215
VERSION AA770215.1 GI:2821453
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 274)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbsr@mail.nih.gov
cDNA Library Preparation: M. Hento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/btrp/image/image.html
Insert Length: 418 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
Location/Qualifiers
1..274
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="1321223"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site: 1: Not I; Site: 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5'
TGTATCCATCTGAAATGGAGCGCGCCGCAATTTTATTTT 3']
(Pharmacia), digested with Not I and Eco RI adaptors
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cots, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
80 a 65 c 57 g 72 t

ORIGIN
Query Match 92.0%; Score 18.4; DB 9; Length 274;
Best Local Similarity 95.0%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
|||||
Db 46 TAATTGCTGTTAATATTTT 27

RESULT 4
AA821323 283 bp mRNA linear EST 17-FEB-1998
LOCUS vs67d07.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
DEFINITION IMAGE:1151341 5', mRNA sequence.
ACCESSION AA821323
VERSION AA821323.1 GI:2891191
KEYWORDS EST.

SOURCE	Mus musculus
ORGANISM	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE	1 (bases 1 to 283)
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisels,S., Kucaba,T., Lacy,M., LeM., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE	The Mashu-HMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project Mashu-HMI Mouse EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNL : contact the IMAGE Consortium (infoimage.llnl.gov) for further information. MGI:624549 Seq primer: -28m13 rev1 ET from Amershams High quality sequence stop: 248. Location/Qualifiers 1..283 /organism="Mus musculus" /strain="C57BL/6" /db_xref="taxon:10090" /cclone_image="1151341" /clone_lib="Stratagene mouse skin (#937313)" /sex="females" /tissue_type="Whole skin" /dev_stage="11 weeks old" /lab_host="SOLR (kanamycin resistant)" /note="Organ: skin; Vector: pBluescript SK-; Site: 1; ECOR: dt. Site:2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCGACGAG 3' -3' adaptor sequence: 5' CTCGACTTTTGTCTTTTTTTT 3'
BASE COUNT	87 a 49 c 53 g 94 t
ORIGIN	
Query Match	92.0%; Score 18.4; DB 9; Length 283;
Best local Similarity	95.0%; Pred. No. 1.7e+03;
Matches 19; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
y	1 TCATTGCTGTATATATTTT 20 1
Db	165 TTATTGCTTAAATATTTT 184
RESULT 5	
LOCUS	BF223892 289 bp mRNA linear EST 30-MAR-2001
DEFINITION	7q36a07.x1 NCI CGAP GC6 Homo sapiens cdv4 clone IMAGE:3700141 3'
VERSION	Similar to SW-GCAP_HUMAN Q07092 COLLAGEN ALPHA 1(XVI) CHAIN
KEYWORDS	PRECURSOR.; ; mRNA sequence.
ACCESSION	BF223892
VERSION	BF223892.1 GI:11131079
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 289) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
JOURNAL	
COMMENT	

FEATURES	source	Location/Qualifiers	1. .289	/organism="Homo sapiens"	
		/db_xref="taxon:9606"			
		/clone_image="3700141"			
		/clone_id="NCI CGAP CG6"			
		/tissue_type="pooled germ cell tumors"			
		/lab_host="DH10B"			
		/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1257096-1258631, 1469064-1470983, and 1475592-1476743).			
		Library distribution by Bento Soares and M. Fatima Bonaldo.			
		info@image.llnl.gov			
FEATURES	source	Location/Qualifiers	1. .289	/organism="Homo sapiens"	
		/db_xref="taxon:9606"			
		/clone_image="3700141"			
		/clone_id="NCI CGAP CG6"			
		/tissue_type="pooled germ cell tumors"			
		/lab_host="DH10B"			
		/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1257096-1258631, 1469064-1470983, and 1475592-1476743).			
		Library distribution by Bento Soares and M. Fatima Bonaldo.			
		info@image.llnl.gov			

```

/clone_1lb-"NCI CGAP GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/noec="vector: pT73D-Pac (Pharmacia) with a modified
polylinker: Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo.

```

Query Match	92.0%	Score 18.4	DB 9	length 298
Best Local Similarity	95.0%	Prod. No. 1.6e+03		
Matches 19; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
1	TGATTCGCTGTAAATATTTT	20		
51	TAAATGCTGTAAATATATTTT	32		

Accession	Result 7	LOCUS	DEFINITION	AI565925	332 bp	mRNA	linear	EST 14-MAY-1999
AI565925/c		LOCUS	AI565925	332 bp	mRNA	linear	EST 14-MAY-1999	
		DEFINITION	tt54h12.x1 NC1_CCAP_pan1 Homo sapiens cDNA clone IMAGE:2226791 3'					
			similar to SW:CAIF_HUMAN 007092 COLLAGEN ALPHA 1(XVI) CHAIN					
			PRECURSOR.; mRNA sequence.					

ACCESSION	AI565925
VERSION	AI565925.1
KEYWORDS	GI:452477
SOURCE	EST ^a .
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. (bases 1 to 312)
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .

JOURNAL COMMENT

unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. consortium/LNL at:
www-bio.llnl.gov/bdnp/image/image.html

Insert Length: 2303 Std. Error: 0.00

Seq Primer: -400p from Gldco

High quality sequence stop: 225

POLYA=No.

FEATURES	SOURCE
Location/Qualifiers	1..332
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:2226791"	
/clone_id="NCI_CGAP_Pan1"	
/tissue_type="adenocarcinoma"	
/lab_host="DH10B"	
/note="Organ: pancreas; Vector: pCMV-Sport6; Site: 1; Salt: Average; Size: 2; Note: Cloned unidirectionally. Primer: Oligo dt. 11348-013"	
BASE COUNT	90 a 82 c 72 g 86 t 2 others
ORIGIN	

Query Match	92.0%;	Score 18.4;	DB 9;	Length 332;
Best Local Similarity	95.0%;	Pred. No. 1.6e+03;		
Matches 19;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
0Y	1	TCATGCTGTATATATTTT	20	

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Db      47 TAATTGCTGTATAATTTT 28
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Accession	LOCUS	DEFINITION	LOCUS	DEFINITION
AA682251/c	AA682251	ah2d11.s1 Soares_testis_HNT Homo sapiens cDNA clone 1293141 3' similar to SW:CA1F_HUMAN 007092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR ;, mRNA sequence.	336 bp	EST 29-DEC-1998

ACCESSION	AA682251	GI:26693833
VERSION	AA682251.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 336)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fátima Bonaalido, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MCL-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/MLNL at: www-bio.llnl.gov/dbp/image/image.html
Insert Length: 285 Std Error: 0.00
Seq primer: -40ml3 fwd: RT from Amersham.

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location/Qualifiers
1..336
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1293141"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGACATGGCAGCCGCCCAATTTTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Hento Soares and M. Fatima Bonaldo. '
BASE COUNT      88 a      84 c      76 g      87 t      1 others
ORIGIN

```

Query Match	92.0%	Score 18.4	DB 9	Length 336
Best Local Similarity	95.0%	Pred. No. 1	6e+03	
Matches 19	Conservative	0	Mismatches 1	Indels 0
Qy	1	TCATTCGCTTAATATTTT	20	
Db	46	TAATTCGCTTAATATTTT	27	

LOCUS	337 bp	MRNA	EST 29-NOV-1999
DEFINITION	x183c10.x1 NCI-CGAP-Pan1 Homo sapiens cDNA clone IMAGE:2681298 3'		
ACCESSION	similar to contains PRT5.t3 PRT5 repetitive element ;, MRNA		
VERSION	sequence.		
KEYWORDS	AM192414.1		
EST.	AM192414.1		
SOURCE	human.		
	GI:6471038		

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 337)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Life Technologies catalog #: 11548-013
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bdrp/image/image.html

FEATURES
 source Possible reversed clone: polyT not found
 Seq primer: -400P from Gibco
 High quality sequence stop: 335.
 Location/Qualifiers
 1..337
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 /db_xref="taxon:9606"
 /clone="IMAGE:2681298"
 /clone_lib="NCI-CGAP_Pan1"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1; Salt:
 Site_2: Not; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.72 kb. Life Technologies catalog #:
 11548-013"

BASE COUNT 89 a 84 c 75 g 88 t 1 others
 ORIGIN

Query Match 92.0%; Score 18.4; DB 10; Length 337;
 Best Local Similarity 95.0%; Pred. No. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
 1 |||||

Db 48 TAAATTCGCTTAATATTTT 29

RESULT 10 339 bp mRNA linear EST 02-MAR-1998
 AA620929
 LOCUS at96402.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1055619
 DEFINITION 3' similar to SM:CAIF.HUMAN Q07092 COLLAGEN ALPHA 1(XVI) CHAIN
 PRECURSOR. ; mRNA sequence.
 AA620929
 ACCSSION AA620929.1 GI:2524868
 VERSION
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 339)
 AUTHORS Hillier,D., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
 Krizman,D., Kucaba,T., Lacey,M., Le,N., Lennon,G., Merra,M., Martin
 J., Moore,B., Scheiblenberg,K., Steptoe,M., Tan,F., Theising,B.,
 White,Y., Wylie,T., Waterson,R. and Wilson,R.
 White, Y., Wylie, T., Waterson, R. and Wilson, R.
 TITLE Washington-NCI human EST Project
 JOURNAL Unpublished (1997)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 297 Std Error: 0.00
 Seq primer: -40m13 fwd. RT from Amersham.

FEATURES
 source Location/Qualifiers
 1..339
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1055619"
 /clone_lib="Soares_testis_NHT"
 /sex="male"
 /lab_host="DH10B"
 /note="Vector: pT73D-pac (pharmacia) with a modified
 polylinker; Site_1: Not; Site_2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech laboratories
 , Inc., and primed with a Not I - Oligo(dt) primer [5'
 TGTACCAATCTGACGAGCGGCGCCCAATTTTTTT 3']
 Double-stranded cDNA was ligated to Eco RI adaptors
 (pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Benito Soares and M. Fatima Bonaldo."

BASE COUNT 93 a 84 c 76 g 86 t
 ORIGIN

Query Match 92.0%; Score 18.4; DB 9; Length 339;
 Best Local Similarity 95.0%; Pred. No. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
 1 |||||

Db 48 TAAATTCGCTTAATATTTT 29

RESULT 11 345 bp mRNA linear EST 29-APR-1999
 A1644998
 LOCUS vs67407.y1 Stragene mouse skin (#937313) Mus musculus cDNA clone
 DEFINITION IMAGE:1151341 5', mRNA sequence.
 A1644998
 ACCSSION A1644998.1 GI:4723473
 VERSION
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 345)
 AUTHORS Merra,M., Hillier,D., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
 B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
 E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterson,R. and Wilson,R.
 TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: Merra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 This read is a RESSEQUENCE of a previously sequenced mouse clone
 correct orientation)
 Seg primer: -40RP from Gibco
 High quality sequence stop: 333.
 Location/Qualifiers
 1..345
 /organism="Mus musculus"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:1151341"
 /clone_lib="Stragene mouse skin (#937313)"
 /sex="females"
 /tissue_type="whole skin"

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/dev-stage="11 weeks old"
/lab-host="SOLR (kenamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; uni-ZAP XR vector; ~5'
adaptor sequence: 5' GAATTCGGCAGCAG 3' ~3' adaptor
sequence: 5' CTCGACTTTTCTTTTCTTTTCTTTT 3' "
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BASE COUNT 120 a 54 c 68 g 103 t

ORIGIN

Query Match 92.0%; Score 18.4; DB 9; Length 345;
Best Local Similarity 95.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
1 |||||||||||||||||||

Db 166 TTAATTCCTGTTAATATTTT 185

RESULT 12
1594048/c 352 bp mRNA linear EST 22-MAR-2000

LOCUS hg44b02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2948427 3'
DEFINITION similar to SW:CAIF_HUMAN 007092 COLLAGEN ALPHA 1(XVI) CHAIN
PRECUSOR. ; mRNA sequence.

ACCESSION AM594048
VERSION AM594048
KEYWORDS EST.
SOURCE AM594048.1 GI:7281306
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 352)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Pimmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI, at:
image.llnl.gov/image/html/tresources.shtml
Seq primer: -400p from Gibco.
Location/Qualifiers
1. 352
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2948427"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA
from the normalized library NCI_CGAP_GC4 was prepared, and
as circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 92 a 88 c 81 g 91 t

ORIGIN

Query Match 92.0%; Score 18.4; DB 10; Length 352;
Best Local Similarity 95.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
1 |||||||||||||||||||

Db 49 TAAATTCCTGTTAATATTTT 30

RESULT 13
AA678445/c 356 bp mRNA linear EST 02-DEC-1997

LOCUS ah01e08.s1 Gessler Wlms tumor Homo sapiens cDNA clone
DEFINITION IMAGE:1155398 3' similar to SW:CAIF_HUMAN 007092 COLLAGEN ALPHA
1(XVI) CHAIN PRECUSOR. ; mRNA sequence.

ACCESSION AA678445
VERSION AA678445
KEYWORDS EST.
SOURCE AA678445.1 GI:2658967
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 356)
Hillier, L., Allen, M., Bowles, L., Dubugue, T., Geisler, G., Jost, S.,
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,
J., Moore, B., Schellenberg, K., Slepecek, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham.
Location/Qualifiers
1. 356
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1155398"
/clone_lib="Gessler Wlms tumor"
/sex="pooled (6)"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; RNA
was prepared from a pool of 6 anonymous Wlms' tumor RNAs.
RNA was prepared by acid-phenol, followed by one round of
oligo dt selection. cDNA library preparation was with
the BRL/Life Tech. Superscript Plasmid system. An
oligo-dt NotI primer for first strand synthesis generated
ggcgccgcctctn at the 3' end of the clones. A 5' SalI
adaptor was used with sequence 5'-gtcagccacagcgacg-3'.
Resulting cDNAs were size selected (average size 2 kb),
NotI digested, and ligated into NotI/SalI-cut pSPORT1.
Library was constructed by Dr. Manfred Gessler."

BASE COUNT 95 a 89 c 84 g 88 t

ORIGIN

Query Match 92.0%; Score 18.4; DB 9; Length 356;
Best Local Similarity 95.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
1 |||||||||||||||||||

Db 43 TAAATTCCTGTTAATATTTT 24

RESULT 14
A1679677/c 382 bp mRNA linear EST 26-MAY-1999

LOCUS tu65c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2255920 3'
DEFINITION similar to SW:CAIF_HUMAN 007092 COLLAGEN ALPHA 1(XVI) CHAIN
PRECUSOR. ; mRNA sequence.

ACCESSION A1679677

```

VERSION      AI679677.1  GI:4889859
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE        1 (bases 1 to 382)
JOURNAL      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished (1997)
              Contact: Robert Strausberg, Ph.D.
              Email: cgabs-r@mail.nih.gov
              Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
              Emmert-Buck, M.D., Ph.D.
              CDNA library preparation: Life Technologies, Inc.
              CDNA library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LINL at:
              www.bio.lnlnl.gov/bdrip/image/image.html
              Seq primer: -40UP from Gibco
              high quality sequence stop: 274.
FEATURES
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    /db_xref="taxon:9606"
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    /lissue_type="poorly differentiated adenocarcinoma with
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    /lab_host="DH10B"
    /note="Organ: stomach; Vector: PCW-SPORT6; Site: 1; Salt;
    Site: 2; Notti; Cloned unidirectionally. Primer: Oligo dt.
    Average insert size 1.69 kb. Life Technologies catalog #:
    11549-011"
BASE COUNT   96 a 98 c 94 g 92 t 2 others
ORIGIN
Query Match 92.0%; Score 18.4; DB 9; Length 382;
Best Local Similarity 95.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCATTGCTGTAATATTTT 20
   1 |||||
Db 44 TAAATGCTGTAATATTTT 25

ESTUT 15
-29062/c
LOCUS       T29062 383 bp mRNA linear EST 06-SEP-1995
DEFINITION  EST, T29062 Human lung Homo sapiens cDNA 3' end similar to collagen,
TYPE       T29062
VERSION    T29062.1
KEYWORDS   T29062.1 GI:611160
SOURCE     EST.
ORGANISM   human.
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult
            C.J., Lee, N., Kitzness, E.F., Weinstein, K.G., Gockayne, J.D., White
            O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A.,
            Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald,
            J.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S.M., Glodex, A.,
            Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkleur, P.S., Kelley, J.M.,
            Klimke, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
            Moreno-Palanges, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M.,
            Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
            Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y.,
            Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J.,
            Dimke, D., Feng, P., Ferrle, A., Fischer, C., Hastings, G.A., He, W.-W.,

```

```

TITLE        Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L.,
              Kunsch, C., Li, H., Li, H., Melsner, P.S., Olsen, H., Raymond, L., Wei
              Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Pannon
              M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
              Venter, J.C.
              Initial Assessment of Human Gene Diversity and Expression Patterns
              Based Upon 83 Million Basepairs of cDNA Sequence
              Nature 377, 3-174 (1995)
              96026280
              Other ESTs: EST67295 THC23485
              Contact: Venter, J.C
              The Institute for Genomic Research
              932 Clopper Rd, Gaithersburg, MD 20878
              Tel: 3018699056
              Fax: 3018699423
              Email: tdbinfo@tdb.tigr.org
              For clone availability, additional sequence and expression
              information related to this EST, please contact the TIGR Database
              (tdbinfo@tdb.tigr.org)
              Seq primer: M13-21.
FEATURES
  source
    1..383
    /organism="Homo sapiens"
    /db_xref="ATCC (lnhost):105192"
    /db_xref="taxon:9606"
    /clone_1b="Human Lung"
    /note="Organ: lung"
BASE COUNT   105 a 86 c 74 g 116 t 2 others
ORIGIN
Query Match 92.0%; Score 18.4; DB 14; Length 383;
Best Local Similarity 95.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCATTGCTGTAATATTTT 20
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Db 42 TAAATGCTGTAATATTTT 23

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Search completed: December 10, 2002, 22:50:14
 Job time : 1029.47 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:03:28 ; Search time 130.391 Seconds
(without alignments)
345.422 Million cell updates/sec

Title: US-09-865-579a-24

Perfect score: 20
Sequence: 1 tcattgcgttaataatttt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

otal number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	ABK85914	Methicillin resist
2	20	100.0	20	ABK85924	Methicillin resist
3	20	100.0	467	AAQ86977	Polynucleotide pro
4	20	100.0	1789	AAQ86977	Staphylococcus aur
5	20	100.0	2007	AAQ86977	Staphylococcus aur
6	20	100.0	2007	AAQ86977	Staphylococcus aur
7	20	100.0	2007	AAQ86977	Staphylococcus aur
8	20	100.0	2007	AAQ86977	Staphylococcus aur
9	20	100.0	2028	ABN92247	Staphylococcus epi

C	10	20	100.0	2110	14	AAQ35213	Sequence of the me
C	11	20	100.0	2322	13	AAQ25905	par2. Synthetic.
C	12	20	100.0	2455	16	AAQ40438	Staphylococcus aur
C	13	20	100.0	2456	22	AAH01187	Staphylococcus aur
C	14	18	90.0	27	19	AAV37097	PCR primer for ant
C	15	17.4	87.0	6987	22	AAQ59566	Human reproductive
C	16	17.4	87.0	6987	22	AAK87097	Human reproductive
C	17	17.4	87.0	6987	23	ABK98520	Human immune/haema
C	18	17	85.0	330	17	ABK98520	Human testicular a
C	19	17	85.0	641	17	AAQ42437	Borrelia lonestari
C	20	17	85.0	641	17	AAQ42437	Borrelia lonestari
C	21	17	85.0	700	22	AAH92320	Human inflammatory
C	22	17	85.0	700	22	AAH92321	Human inflammatory
C	23	17	85.0	805	16	AAQ83839	Borrelia lonestari
C	24	16.8	84.0	918	24	ABK68234	Streptococcus poly
C	25	16.8	84.0	2119	24	AAQ31696	Mouse CD39L4 CDNA.
C	26	16.8	84.0	17687	22	AAQ42069	Genomic sequence #
C	27	16.8	84.0	19815	22	AAQ42064	Genomic sequence #
C	28	16.8	84.0	20746	22	AAQ73553	Human reproductive
C	29	16.8	84.0	22635	22	AAQ72203	Human reproductive
C	30	16.8	84.0	32191	22	AAQ26704	Human genomic DNA
C	31	16.8	84.0	49561	22	AAK82012	Human immune/haema
C	32	16.8	84.0	50885	22	AAK70336	Human immune/haema
C	33	16.8	84.0	213251	24	AAQ67193	Listeria innocua c
C	34	16.8	84.0	640681	24	AAQ92787	Buchnera sp. genom
C	35	16.8	82.0	220	13	AAQ20723	B.hernesi strain Y
C	36	16.4	82.0	220	13	AAQ20724	Specifically ampli
C	37	16.4	82.0	220	13	AAQ20725	Specifically ampli
C	38	16.4	82.0	863	22	AAH72981	Human cervical can
C	39	16.4	82.0	1005	13	AAQ20721	B.hernesi HSL flag
C	40	16.4	82.0	1433	23	AAQ88979	DNA encoding novel
C	41	16.4	82.0	1449	23	AAQ93004	DNA encoding novel
C	42	16.4	82.0	2964	23	AAI24732	Drosophila melanog
C	43	16.4	82.0	3924	23	AAQ75372	DNA encoding novel
C	44	16.4	82.0	3924	23	AAQ75372	DNA encoding novel
C	45	16.4	82.0	3924	23	AAQ75372	DNA encoding novel

ALIGNMENTS

RESULT 1
ID ABK85914 standard; DNA: 20 BP.
AC ABK85914:
XX
DF 16-AUG-2002 (first entry)
XX
DE Methicillin resistant Staphylococcus aureus detection primer #14.
XX
XX Methicillin resistant Staphylococcus aureus; MRSA; primer: ss;
KM meca; probe.
XX
XX
OS Staphylococcus aureus.
XX
XX
PN EP160333-A2.
XX
PD 05-DEC-2001.
XX
PF 29-MAY-2001: 2001EP-0112100.
XX
PR 29-MAY-2000: 2000JP-0163149.
PR 09-JUN-2000: 2000JP-0179394.
XX
PA (TOYD) TOSOH CORP.
XX
PI Taya T, Ishiguro T, Saito J;
XX
DR WPI; 2002-395832/43.
XX
PT New oligonucleotide specific for the meca methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related


```

PT mRNA -
XX
XX Claim 1; Page 17; 28pp; English.
PS
XX This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the meca gene (associated with methicillin resistance in
CC Staphylococcus aureus) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the meca gene as template. Also disclosed is a detection
CC method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant S. aureus in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the meca gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC Staphylococcus aureus (MRSA) detection oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 2 C; 2 G; 12 T; 0 other;

Query Match          100.0%; Score 20; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATTGCTGTTAATATTTT 20
   |||||||
DB 1 TCATTGCTGTTAATATTTT 20

RESULT 2
ABK85924
ID ABK85924 standard; DNA; 20 BP.
XX
XX ABK85924;
AC
XX
XX 16-AUG-2002 (first entry)
DT
XX
XX Methicillin resistant Staphylococcus aureus detection primer #24.
DE
XX Methicillin resistant Staphylococcus aureus; MRSA; primer; ss;
KW meca; probe.
XX
XX Staphylococcus aureus.
NS
? EPI160333-A2.
XX
XX 05-DEC-2001.
PD
XX
XX 29-MAY-2001; 2001EP-0112100.
PF
XX
XX 29-MAY-2000; 2000JP-0163149.
PR
XX 09-JUN-2000; 2000JP-0179394.
XX
XX (TOYO ) TOSOH CORP.
PA
XX
XX Taya T, Ishiguro T, Saito J;
PI
XX
XX WPI; 2002-395832/43.
DR
XX
XX New oligonucleotide specific for the meca methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related
PT mRNA -
XX
XX Claim 5; Page 20; 28pp; English.
PS
XX This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the meca gene (associated with methicillin resistance in

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CC Staphylococcus aureus) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the meca gene as template. Also disclosed is a detection
CC method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant S. aureus in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the meca gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC Staphylococcus aureus (MRSA) detection oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 2 C; 2 G; 12 T; 0 other;

Query Match          100.0%; Score 20; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. NO. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCATTGCTGTTAATATTTT 20
   |||||||
DB 1 TCATTGCTGTTAATATTTT 20

RESULT 3
AAQ86977/c
ID AAQ86977 standard; DNA; 467 BP.
XX
XX AAQ86977;
AC
XX
XX 16-JAN-1996 (first entry)
DT
XX
XX Polynucleotide probe for methicillin resistant Staphylococcus aureus.
DE
XX
XX MRSA; methicillin resistant Staphylococcus aureus; probe;
KW hybridisation; meca; MRSE; Staphylococcus epidermis; ss.
XX
XX Staphylococcus aureus.
OS
XX
XX DE4338119-A1.
PN
XX
XX 11-MAY-1995.
PD
XX
XX 08-NOV-1993; 93DE-4338119.
PF
XX
XX 08-NOV-1993; 93DE-4338119.
PR
XX
XX (FARB ) BAYER AG.
PA
XX
XX Endermann R, Springer W;
PI
XX
XX WPI; 1995-180108/24.
DR
XX
XX Detection of methicillin resistant Staphylococcus - using an
PT oligo:nucleotide derived from the meca gene
PT
XX
XX Claim 2; Page 11; 14pp; German.
PS
XX
XX An oligonucleotide probe having the 467 nucleotide sequence shown
CC isolated from S. aureus, is capable of hybridising with the DNA or
CC RNA of methicillin resistant S. aureus (MRSA). The probe is
CC specifically derived from the meca gene of S. aureus and S. epidermidis.
CC The meca gene product has no homology with known PBPs
CC (penicillin-binding proteins). The new probes allow for the rapid
CC identification of all MRSA, eradicated need for labour intensive in
CC vitro cultivation and physiological assays.
XX
XX Sequence 467 BP; 187 A; 73 C; 85 G; 122 T; 0 other;

```


KM Haemophilus influenzae; Moraxella catarrhalis; septicæmia; meningitis;
 KM infection: intra-abdominal infection; skin infection;
 KM bacterial resistance; beta-lactam antibiotic; ds.
 XX
 OS Synthetic.
 XX
 PN MO9608582-A2.
 XX
 PD 21-MAR-1996.
 XX
 PF 12-SEP-1995; 95MO-CA00528.
 XX
 PR 12-SEP-1994; 94US-0304732.
 XX
 PA (BERG/) BERGERON M G.
 PA (OUEL/) OUELLETTE M.
 XX (ROY/P/) ROY P H.
 PI Bergeron MG, Ouellette M, Roy PH;
 XX
 R WPI; 1996-179953/18.
 T Method for the detection of bacterial species using probes and
 PT primers - allows detection and quantification of antibiotic
 PT resistant bacteria in patients, the environment and food
 XX
 PS Claim 91; Page 144-145; 216pp; English.
 XX
 CC The sequences given in AAT28560-76 represent fragments derived from
 CC bacterial antibiotic resistance genes which were used as probes in the
 CC method of the invention for the detection of bacterial species in a
 CC sample. The method of the invention comprises using probes and/or
 CC amplification primers which are specific, ubiquitous and sensitive for
 CC determining the presence and/or amount of nucleic acids from selected
 CC bacterial species in any sample, where the bacterial nucleic acid
 CC comprises a selected target region hybridisable with the probes or
 CC primers. The method comprises contacting the sample with the probes
 CC or primers and detecting the presence and/or amount of hybridised
 CC primers or amplification products as and indication of the presence
 CC and/or amount of the bacterial species. This method may be used to
 CC detect commonly encountered bacterial pathogens, e.g. Escherichia coli,
 CC Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis,
 CC Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus
 CC enterodermidis, Enterococcus faecalis, Staphylococcus saprophyticus,
 CC Streptococcus pyogenes, Haemophilus influenzae and Moraxella
 CC catarrhalis. These bacterial species are associated with approx. 90% of
 CC urinary tract infections and with a high percentage of other severe
 CC infections including septicæmia, meningitis, pneumonia, intra-abdominal
 CC infections, skin infections and other severe respiratory tract
 CC infections. The method may also be used to evaluate a bacterial
 CC resistance to beta-lactam antibiotics.
 XX
 SQ Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
 XX
 QY Query Match 100.0%; Score 20; DB 17; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 1234 TCATTGCTGTTAATATTTT 20
 1234 TCATTGCTGTTAATATTTT 1215

RESULT 7
 ID AAV68337/C
 XX AAV68337 standard; DNA; 2007 BP.
 AC AAV68337;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Penicillin binding protein PBP2A meca-27R gene of S. aureus 27R.
 XX

KM Penicillin binding protein; PBP2A-27A; meca-27R gene;
 KM methicillin resistance; antibiotic; assay; purification; ss.
 XX
 OS Staphylococcus aureus.
 XX
 PN EP875578-A2.
 XX
 PD 04-NOV-1998.
 XX
 PF 18-MAR-1992; 92EP-0302298.
 XX
 PR 19-MAR-1991; 91US-0672704.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Blaszcak LC, Skatrud PL, Smith MC, Wu CE;
 XX
 DR WPI; 1998-559443/48.
 DR P-PSDB; AAW81149.
 XX
 PT New Staphylococcus aureus soluble penicillin-binding proteins and
 PT their derivatives - useful for screening for compounds effective
 PT against methicillin resistant organisms
 XX
 PS Disclosure; Page 14-16; 97pp; English.
 XX
 CC This meca-27R gene encodes penicillin binding protein 2A (PBP2A-27R)
 CC responsible for the methicillin resistance of Staphylococcus aureus
 CC strain 27R. The invention provides new PBPs of formula SP-L-PBP2As,
 CC where: SP is 0 or a signal peptide (preferably from the ampC, ompA or
 CC beta-lactamase gene product); L is Met-Val or a compound of formula
 CC Met-Gly-CP-(Pro)n-PBP2As, where CP = 0 or a chelating peptide (see
 CC AAW81151-58) of formula (His)x-(A)y-(His)z and A=an amino acid,
 CC x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above
 CC polypeptide where each monomer unit is the same or different; Pro
 CC is proline, n = 0 or 1; and PBP2As is soluble PBP2A-27R protein (see
 CC AAW81159-62). Also claimed are polynucleotides encoding specific
 CC soluble PBP2A compounds. The new PBP2A-27R proteins are useful for
 CC assaying for agents useful as antibiotics against methicillin
 CC resistant Staphylococcus strains by creating a kinetically inert
 CC complex between a support-immobilised transition ion and a modified
 CC soluble PBP2A protein comprising a chelating agent, which screens
 CC for agents which bind to PBP2A proteins (disclosed). Soluble forms
 CC of PBP2A-27R protein facilitate crystallisation as they lack their
 CC transmembrane association region, and so are useful for x-ray
 CC crystallography studies of the protein, assisting in the design of
 CC antibiotic compounds against methicillin resistant Staphylococcus
 CC strains (disclosed). The chelating peptide operably linked to the
 CC PBP2A-27R proteins is useful for purifying PBPs.
 XX
 SQ Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
 XX
 QY Query Match 100.0%; Score 20; DB 19; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 1234 TCATTGCTGTTAATATTTT 20
 1234 TCATTGCTGTTAATATTTT 1215

RESULT 8
 ID ABA76993/C
 XX ABA76993 standard; DNA; 2007 BP.
 AC ABA76993;
 XX
 DT 28-JAN-2002 (first entry)
 XX
 DE Antibiotic resistance detection polynucleotide SEQ ID NO 169.
 XX
 DE Detection; bacterial species; animal; food; environment;
 KM antibiotic resistance; ds.
 KM

```

XX OS Unidentified.
XX PN NZ501596-A.
XX PD 29-JUN-2001.
XX PF 12-SEP-1995: 95NZ-0501596.
XX PR 12-SEP-1995: 95NZ-0501596.
XX PA (ID11-) IDI INPECTIO DIAGNOSTIC INC.
XX PI Bergeron MG, Ouellette M, Roy PH;
XX DR MPI: 2001-615034/71.
XX PT Method for detecting target bacterial species in a sample, comprises
XX T detecting the presence or amount of bacterial nucleic acid amplified by
XX f a primer derived from bacterial DNA, specific for the target bacterial
XX f species.
XX PS Claim 16: Page 159-160; 168pp; English.
XX CC The invention relates to detecting target bacterial species suspected to
XX CC be present in a sample, comprising contacting nucleic acids of target
XX CC bacterial species with an amplification primer pair derived from a
XX CC bacterial DNA fragment (ABA76825-ABA76861) specific for the target
XX CC bacterial species but ubiquitous for different strains, amplifying the
XX CC nucleic acid and detecting the presence or amount of an amplified
XX CC sequence as an indication of the presence or amount of the target
XX CC bacterial species. The invention includes primers and probes
XX CC (ABA76862-ABA76984) against the target bacterial species, especially
XX CC E.coli, K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae,
XX CC S.aureus, S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes,
XX CC H.influenzae, M.cattarrhalis and/or group A Streptococci producing
XX CC exotoxin A gene spe A, suspected to be present in a sample which is
XX CC obtained from human patients, animals, environment or food, and which
XX CC consists of one or more bacterial colonies. Oligonucleotide
XX CC probes and primers complementary to the bacterial genes encoding
XX CC resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aadB,
XX CC aac(1), aac(2), aac(3), aac(4), mecA, vanA, vanH, vanX, aacA-aphD, vat,
XX CC vga, msrA, sul and/or int (ABA76985-ABA77001) are also useful to identify
XX CC commonly encountered and clinically important resistance genes. The
XX CC invention provides a rapid method of bacterial identification that can be
XX CC achieved, which reduces the time currently required for the
XX CC identification of pathogens in the clinical laboratory.
XX Q Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
XX
XX Query Match 100.0%; Score 20; DB 22; Length 2007;
XX Best Local Similarity 100.0%; Pred. No. 27;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 TCATTGCTGTTAATATATTTT 20
XX |||||||||||||||||||
XX Db 1234 TCATTGCTGTTAATATATTTT 1215
XX
XX RESULT 9
XX ABN92247/c
XX ID ABN92247 standard; DNA; 2028 BP.
XX AC
XX AC ABN92247;
XX XX
XX DT 24-JUL-2002 (first entry)
XX XX
XX DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1710.
XX XX
XX KM Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
XX KM antibacterial; gene therapy; gene; ds.
XX XX
XX OS Staphylococcus epidermidis.

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XX PN US6380370-B1.
XX XX
XX PD 30-APR-2002.
XX XX
XX PF 13-AUG-1998; 98US-0134001.
XX XX
XX PR 14-AUG-1997: 97US-055779P.
XX PR 08-NOV-1997: 97US-064964P.
XX XX
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Doucette-Stamm LA, Bush D;
XX PT
XX DR MPI: 2002-381255/41.
XX DR P-PSDB; ABP39702.
XX PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
XX PT polypeptide, useful for diagnosing and treating bacterial infections -
XX PS Disclosure; SEQ ID 1710; 267pp; English.
XX XX
XX CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
XX CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
XX CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
XX CC antibacterial activity and can be used in gene therapy. The sequences
XX CC can also be used in the diagnosis and treatment of bacterial infections,
XX CC particularly S. epidermidis infections. The sequences can be used to
XX CC screen for compounds able to interfere with the S. epidermidis life
XX CC cycle or inhibit S. epidermidis infection.
XX CC N.B. The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from the
XX CC USPTO web site.
XX SO Sequence 2028 BP; 861 A; 273 C; 346 G; 547 T; 1 other;
XX
XX Query Match 100.0%; Score 20; DB 24; Length 2028;
XX Best Local Similarity 100.0%; Pred. No. 27;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 TCATTGCTGTTAATATATTTT 20
XX |||||||||||||||||||
XX Db 1255 TCATTGCTGTTAATATATTTT 1236
XX
XX RESULT 10
XX AAQ35213/c
XX ID AAQ35213 standard; DNA; 2110 BP.
XX AC
XX AC AAQ35213;
XX XX
XX DT 06-JUN-1993 (first entry)
XX XX
XX DE Sequence of the mec A gene.
XX XX
XX KM Methicillin-resistant staphylococci; detection; primer; PCR; ss.
XX OS Staphylococcus aureus.
XX XX
XX FH Key Location/Qualifiers
XX FT CDS 105..2110
XX FT /*tag= a
XX PN EP527628-A.
XX XX
XX PD 17-FEB-1993.
XX XX
XX PF 10-AUG-1992; 92EP-0307307.
XX XX
XX PR 13-AUG-1991: 91US-0744770.
XX XX
XX PA (ELIL ) LILLY & CO ELI.
XX XX

```

```
P1 Skatrud PL, Unal S;
XX
DR WPI: 1993-054352/07.
DR P-PSDB: AAR30845.
XX
PT Detection of methicillin-resistant staphylococci - using
PT polymerase chain reaction method, and DNA primers, for rapid,
PT sensitive and accurate detection
XX
PS Disclosure: Pages 7-10; 16pp; English.
XX
CC The inventors claim a method for detecting methicillin-resistant
CC staphylococcal infections which involves the use of the PCR primed
CC by fragments of the Staphylococcus meca gene. More specifically, the
CC initial primers used are nucleotides 141-160 and the inverse
CC complement of nucleotides 1929-1952 of the S. aureus meca gene. The
CC interior primers are nucleotides 568-593 and the inverse complement
CC of 1647-1670 of the S. aureus meca gene.
XX
SQ Sequence 2110 BP; 896 A; 290 C; 350 G; 574 T; 0 other;
Query Match 100.0%; Score 20; DB 14; Length 2110;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCATTGCTGCTTAATATTTT 20
DB 1338 TCATTGCTGCTTAATATTTT 1319
RESULT 11
AAQ25905/C
ID AAQ25905 standard; DNA; 2322 BP.
XX
AC AAQ25905;
XX
DT 18-JAN-1993 (first entry)
XX
DE PBP2'.
XX
KW Polymerase chain reaction; PCR; amplification; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 1581..1598
FT /tag= a
FT /label= Probe_binding_site
XX
JP04169200-A.
XX
17-JUN-1992.
XX
PF 31-OCT-1990; 90JP-0296708.
XX
PR 31-OCT-1990; 90JP-0296708.
XX
PA (SHIO ) SHIONOGI & CO LTD.
XX
DR WPI: 1992-253403/31.
XX
PT Detection of PBP2' gene for determ. of methicillin-resistance -
PT useful esp. for detection of methicillin-resistance
PT Staphylococcus aureus
XX
PS Disclosure: Fig 1; 9pp; Japanese.
XX
CC The sequence given is the PBP2' gene. This gene could be detected
CC by the primer sequences given in AAQ25905-904. Due to the results of
CC this amplification reaction resistance to methicillin in Staphylococcus
CC aureus could be determined.
XX
SQ Sequence 2322 BP; 940 A; 324 C; 389 G; 669 T; 0 other;
```

```
Query Match 100.0%; Score 20; DB 13; Length 2322;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCATTGCTGCTTAATATTTT 20
DB 1240 TCATTGCTGCTTAATATTTT 1221
RESULT 12
AAT04538/C
ID AAT04538 standard; CDNA to mRNA; 2455 BP.
XX
AC AAT04538;
XX
DT 11-APR-1996 (first entry)
XX
DE Staphylococcus aureus meca protein coding sequence.
XX
KW methicillin-resistant Staphylococcus aureus; MRSA; 'meca' protein;
KW antibiotic resistance; ds.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT CDS 134..2146
FT /tag= a
FT /product= mec_A-protein
XX
JP07209294-A.
XX
PD 11-AUG-1995.
XX
PF 10-JAN-1994; 94JP-0012226.
XX
PR 10-JAN-1994; 94JP-0012226.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KAWA/) KAWANO M.
PA (MITU ) MITSUBISHI CHEM CORP.
XX
DR WPI: 1995-313917/41.
DR P-PSDB: AAR80036.
XX
PT New 'mec A' protein and DNA encoding it - used for the detection of
PT methicillin-resistant Staphylococcus aureus
XX
PS Example 2; Page 8-10; 15pp; Japanese.
XX
CC The present sequence codes for the mec A protein. DNA coding for
CC the 'mec A' protein, which controls methicillin resistance in
CC methicillin-resistant Staph. aureus (MRSA), was obtained by PCR
CC amplification of the mec A sequence using primers AAT04537 and
CC AAT04539. The 'mec A' protein (mol. wt. 40000) is useful for
CC preparation of antiserum specific for MRSA, thereby allowing
CC methicillin-resistant and methicillin-sensitive strains to be
CC distinguished.
XX
SQ Sequence 2455 BP; 997 A; 344 C; 401 G; 713 T; 0 other;
Query Match 100.0%; Score 20; DB 16; Length 2455;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCATTGCTGCTTAATATTTT 20
DB 1373 TCATTGCTGCTTAATATTTT 1354
RESULT 13
AAH01187/C
ID AAH01187 standard; DNA; 2456 BP.
```

```

XX AC AAH01187;
XX DT 24-JUL-2001 (first entry)
XX DE Staphylococcus aureus nucleotide sequence SEQ ID NO:1178.
XX
XX KM Species specific; genus specific; family specific; probe; detection;
XX KM Identification; algal; archaeal; bacterial; fungal; parasitica;
XX KM microorganism; diagnosis; translation elongation factor fu; toxin;
XX KM translation elongation factor G; RecA recombinase; resistance;
XX KM catalytic subunit of proton-translocating ATPase; antimicrobial;
XX KM vaccine; primer; ds.
XX
XX OS Staphylococcus aureus.
XX
XX PN W0200123604-A2.
XX
XX PD 05-APR-2001.
XX
XX 28-SEP-2000; 2000MO-CA01150.
XX
XX 28-SEP-1999; 99CA-2283458.
XX 19-MAY-2000; 2000CA-2307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (ID1) INC.
XX
XX PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
XX PI Picard FJ, Roy PH;
XX
XX DR WPI; 2001-245006/25.
XX
XX PT Nucleic acid sequences are used to generate universal probes and
XX PT primers which can be used to identify and detect the presence of algal,
XX PT archaeal, bacterial, fungal and parasitica species in a test sample -
XX
XX PS Disclosure: Page 1048-1049; 1580pp; English.
XX
XX CC The present invention describes a method for generating a repertoire of
XX CC nucleic acids of tuf, fts, atpD and/or recA genes from which probes
XX CC and/or primers are derived. The method comprises amplifying the nucleic
XX CC acids of determined algal, archaeal, bacterial, fungal and parasitica
XX CC species with a combination of defined primer pairs. The method can be
XX CC used for producing probes and/or primers for detecting one or more
XX CC related microorganisms e.g. algae, archaea, bacteria, fungi and
XX CC parasites, for universal detection and for specific and ubiquitous
XX CC detection and identification of an algal, archaeal, bacterial, fungal
XX CC and parasitica species, genus, family and group. A nucleic acid (I)
XX CC obtained using the method of the invention can be used for the universal
XX CC detection of any bacterium, fungus or parasite in a sample and for the
XX CC detection of at least one antimicrobial agent resistance gene or at
XX CC least one toxin gene. hea nucleic acids are used for the specific and
XX CC ubiquitous detection and for identification of Streptococcus pneumoniae.
XX CC (I) can be used to design a therapeutic agent which is effective against
XX CC microorganisms. Microbial species or genus or family or phylum or group
XX CC which can be detected include Abiotrophia adhaerens, Bordetella sp.,
XX CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
XX CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp.,
XX CC Neisseria gonorrhoeae and Staphylococcus sp.. using DNA based tests
XX CC provides faster results than substrate specificity tests as results can
XX CC be determined in an hour and improved accuracy is also achieved.
XX CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
XX CC which are given in the exemplification of the present invention.
XX
XX SQ Sequence 2456 BP; 1001 A; 344 C; 396 G; 715 T; 0 other.
XX
XX Query Match 100.0%; Score 20; DB 22; Length 2456;
XX Best Local Similarity 100.0%; Pred. No. 27;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TCATGCTGTTAATATTTT 20
XX |||||||||||||||||||
XX DB 1374 TCATGCTGTTAATATTTT 1355

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XX RESULT 14
XX AAV37097
XX ID AAV37097 standard; DNA; 27 BP.
XX
XX AC AAV37097;
XX
XX DT 04-SEP-1998 (first entry)
XX DE PCR primer for antibiotic resistance gene mecA.
XX
XX KM Detection; bacterial antibiotic resistance gene; bacteria;
XX KM fungal species; identification; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX PN W09820157-A2.
XX
XX PD 14-MAY-1998.
XX
XX 04-NOV-1997; 97MO-CA00829.
XX
XX 04-NOV-1996; 96US-0743637.
XX
XX (ID11-) ID1 INFECTIO DIAGNOSTIC INC.
XX
XX PI Bergeron MG, Ouellette M, Picard FJ, Roy PH;
XX PI WPI; 1998-286967/25.
XX
XX DR WPI; 1998-286967/25.
XX
XX PT Use of oligo:nucleotide primers and probes - for detection,
XX PT identification and quantification of bacteria, fungi and bacterial
XX PT antibiotic resistance gene(s)
XX
XX PS Claim 21; Page 103; 167pp; English.
XX
XX CC PCR primers AAV37096-97 are used to amplify antibiotic resistance gene
XX CC mecA. They are used in the course of the invention. The specification
XX CC describes the use of probes and/or amplification primers which are
XX CC specific, ubiquitous and sensitive for determining the presence and
XX CC amount of nucleic acids from a bacterial antibiotic resistance gene
XX CC and specific bacterial and fungal species in any sample suspected of
XX CC containing the bacterial or fungal nucleic acids, where each of the
XX CC nucleic acid or variant or part comprises a selected target region
XX CC hybridisable with the probes or primers. The method of use comprises
XX CC contacting the sample with the probes or primers and detecting the
XX CC presence of hybridised probes or amplified products as an indication
XX CC of the presence of the specific bacterial or fungal species and
XX CC bacterial antibiotic resistance genes. The methods and products can
XX CC be used to detect and identify the bacterial and fungal species and
XX CC genera and determine the bacterial resistance to antibiotics.
XX
XX SQ Sequence 27 BP; 7 A; 1 C; 5 G; 14 T; 0 other.
XX
XX Query Match 90.0%; Score 18; DB 19; Length 27;
XX Best Local Similarity 100.0%; Pred. No. 1,8e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 ATTGCTGTTAATATTTT 20
XX |||||||||||||||||||
XX DB 1 ATTGCTGTTAATATTTT 18
XX
XX RESULT 15
XX AAL05956/C
XX ID AAL05956 standard; DNA; 6987 BP.
XX
XX AC AAL05956;
XX
XX DT 21-NOV-2001 (first entry)
XX DE Human reproductive system related antigen DNA SEQ ID NO: 8644.

```

XX Human: reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200155320-A2.
PD
XX 02-AUG-2001.
PE
XX 17-JAN-2001; 2001WO-US01339.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232387.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.

PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251889.
PR 08-DEC-2000; 2000US-0251990.

PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI: 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen
PT is used in preventing, treating or ameliorating a medical condition -
XX
XX
XX Disclosure; SEQ ID NO 8644; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention.
Y
Y Sequence 6987 BP; 1740 A; 1642 C; 1626 G; 1979 T; 0 other:
Query Match 87.0%; Score 17.4; DB 22; Length 6987;
Best Local Similarity 94.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 TCATTGCTGTATAATTT 19
|||||
Db 197 TCATTGCTGTATAATTT 179

Search completed: December 10, 2002, 17:32:40
Job time : 132.391 secs

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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 : Search time 27.2626 Seconds

(without alignments)
224.980 Million cell updates/sec

Title: US-09-865-579A-23

Sequence: 1 tttctttttatcttcgttla 20

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

al number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_MA:*
2: /cgn2_6/plodata/1/ina/5A.COMB.seq:*
3: /cgn2_6/plodata/1/ina/5B.COMB.seq:*
4: /cgn2_6/plodata/1/ina/6A.COMB.seq:*
5: /cgn2_6/plodata/1/ina/6B.COMB.seq:*
6: /cgn2_6/plodata/1/ina/PCFUS.COMB.seq:*
7: /cgn2_6/plodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	2007	2	US-08-743-637B-169
2	20	100.0	2007	3	US-08-526-840B-169
3	20	100.0	2028	4	US-09-134-001C-1710
4	16.8	84.0	30549	4	US-09-134-001C-322
5	16.4	82.0	267	2	US-09-134-001C-1218
6	15.8	79.0	1820	2	US-08-757-046A-4
7	15.8	79.0	1820	3	US-09-447-208-4
8	15.8	79.0	1820	3	US-09-135-988-4
9	15.8	79.0	1820	3	US-09-277-716-4
10	15.8	79.0	1820	4	US-08-597-274A-4
11	15.8	79.0	1820	4	US-08-908-909-4
12	15.8	79.0	1820	4	US-09-609-161B-4
13	15.8	79.0	1820	4	US-08-990-103-4
14	15.8	79.0	3033	1	US-08-003-311B-1
15	15.8	79.0	3033	1	US-08-261-432-1
16	15.8	79.0	3145	4	US-09-221-017B-855
17	15.8	79.0	4692	4	US-08-961-527-220
18	15.8	79.0	5630	2	US-08-937-931-1
19	15.8	79.0	5630	4	US-09-285-502-1
20	15.8	79.0	5630	4	US-09-709-126-1
21	15.8	79.0	5630	4	US-09-871-385A-1
22	15.8	79.0	5873	1	US-07-928-464-4
23	15.8	79.0	5873	5	PCT-US93-07347-4
24	15.8	79.0	5890	1	US-07-928-464-3
25	15.8	79.0	5890	1	US-07-928-464-5
26	15.8	79.0	5890	1	US-07-928-464-6
27	15.8	79.0	5890	5	PCT-US93-07347-3

28	15.8	79.0	5890	5	PCT-US93-07347-5	Sequence 5, Appli
29	15.8	79.0	5890	5	PCT-US93-07347-6	Sequence 6, Appli
30	15.8	79.0	6295	1	US-08-003-311B-4	Sequence 4, Appli
31	15.8	79.0	6295	1	US-08-261-432-4	Sequence 4, Appli
32	15.8	79.0	6312	1	US-08-003-311B-3	Sequence 3, Appli
33	15.8	79.0	6312	1	US-08-003-311B-5	Sequence 5, Appli
34	15.8	79.0	6312	1	US-08-003-311B-6	Sequence 6, Appli
35	15.8	79.0	6312	1	US-08-003-311B-7	Sequence 7, Appli
36	15.8	79.0	6312	1	US-08-261-432-3	Sequence 3, Appli
37	15.8	79.0	6312	1	US-08-261-432-5	Sequence 5, Appli
38	15.8	79.0	6312	1	US-08-261-432-6	Sequence 6, Appli
39	15.8	79.0	6312	1	US-08-261-432-7	Sequence 7, Appli
40	15.8	79.0	169998	4	US-09-676-610B-24	Sequence 24, Appli
41	15.4	77.0	834	4	US-09-134-001C-2775	Sequence 2775, Ap
42	15.4	77.0	9919	3	US-08-880-179-1	Sequence 1, Appli
43	15.4	77.0	19250	4	US-08-961-527-35	Sequence 35, Appli
44	15.4	77.0	43676	3	US-09-356-952-12	Sequence 12, Appli
45	15.2	76.0	562	3	US-09-038-909-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-743-637B-169/C
Sequence 169, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: COULETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/743,637B
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0%; Score 20; DB 2; Length 2007;

Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCTTTTATCTCGGTTA 20
Db 1167 TTTCTTTTATCTCGGTTA 1148

RESULT 2
US-08-526-840B-169/c
Sequence 169, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: APPLICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESSES:
ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
08-526-840B-169

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 2007;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCTTTTATCTCGGTTA 20
Db 1167 TTTCTTTTATCTCGGTTA 1148

RESULT 3
US-09-134-001C-1710/c
Sequence 1710, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucelle-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1710
LENGTH: 2028
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
FEATURE:
NAME/KEY: unsure
LOCATION: (52)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 2028;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCTTTTATCTCGGTTA 20
Db 1188 TTTCTTTTATCTCGGTTA 1169

RESULT 4
US-09-134-001C-322/c
Sequence 322, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucelle-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 322
LENGTH: 30549
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-322

Query Match
Best Local Similarity 84.0%; Score 16.8; DB 4; Length 30549;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TTTCTTTTATCTCGGTTA 20
Db 22626 TTTCTTTTATCTCGGTTA 22607

RESULT 5
US-09-134-001C-1218/c
Sequence 1218, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucelle-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
SEQ ID NO: 1218
LENGTH: 267
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1218

Query Match 82.0%; Score 16.4; DB 4; Length 267;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CTTTTCCTTCCTTCA 20
DB 49 CTTTTCCTTCCTTCA 32

RESULT 6
US-08-757-046A-4/C
Sequence 4, Application US/08757046A
Patent No. 5876995

GENERAL INFORMATION:

APPLICANT: Bryan, Bruce
TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,046A
FILING DATE: 11-25-96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,274
FILING DATE: 02-06-96
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE//DOCKET NUMBER: 6680-105B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062

TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1820 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1664
OTHER INFORMATION: Vargula (cypridina) luciferase
PUBLICATION INFORMATION:
AUTHORS: Thompson et al.
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 86
PAGES: 1326-1332
DATE: (1989)
DOCUMENT NUMBER: JP 3-30678 Osaka (Tsuji)

Query Match 79.0%; Score 15.8; DB 2; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTTCCTTCCTTCA 19
DB 1719 TTTTTCCTTCCTTCA 1701

RESULT 7
US-09-447-208-4/C
Sequence 4, Application US/09447208
Patent No. 611386

GENERAL INFORMATION:

APPLICANT: Bryan, Bruce
TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Erman White & McAlliff
STREET: 4250 Executive Square, 7th floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/447,208
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0909/135,988
FILING DATE: 08-17-98
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/757,046
FILING DATE: 11-25-96
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,274
FILING DATE: 02-06-96
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE//DOCKET NUMBER: 24727-105C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-450-8499

TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1820 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1664
OTHER INFORMATION: Vargula (cypridina) luciferase
PUBLICATION INFORMATION:
AUTHORS: Thompson et al.
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 86
PAGES: 1326-1332
DATE: (1989)
DOCUMENT NUMBER: JP 3-30678 Osaka (Tsuji)

Query Match 79.0%; Score 15.8; DB 3; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGCTT 19
|||||
Db 1719 TTCTTTTATCTTCGCT 1701

RESULT 8
US-09-135-988-4/c

Sequence 4, Application US/09135988

Patent No. 6152358

GENERAL INFORMATION:

APPLICANT: Bryan, Bruce

TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: Heller Ehrman White & McCauliffe

STREET: 4250 Executive Square, 7th Floor

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/135,988

FILING DATE:

CLASSIFICATION:

PRIORITY INFORMATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/757,046

FILING DATE: 11-25-96

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/597,274

FILING DATE: 02-06-96

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 24727-105C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-450-8400

TELEFAX: 619-450-8499

FLEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1820 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1..1664

OTHER INFORMATION: Vargula (cypridina) Luciferase

PUBLICATION INFORMATION: JP 3-30678 Osaka (Tsuji)

AUTHORS: Thompson et al.

JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

VOLUME: 86

PAGES: 1326-1332

DATE: (1989)

US-09-135-988-4

Query Match 79.0%; Score 15.8; DB 3; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGCTT 19
|||||
Db 1719 TTCTTTTATCTTCGCT 1701

RESULT 9
US-09-277-716-4/c

Sequence 4, Application US/09277716A

Patent No. 6232107

GENERAL INFORMATION:

APPLICANT: Bryan, Bruce

APPLICANT: Szent-Gyorgyi, Christopher

APPLICANT: PROLOME, LTD.

TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE

CURRENT APPLICATION NUMBER: US/09/277,716A

EARLIER FILING DATE: 1999-03-26

EARLIER APPLICATION NUMBER: 60/102,939

EARLIER FILING DATE: 1998-10-01

EARLIER APPLICATION NUMBER: 60/089,367

EARLIER FILING DATE: 1998-06-15

EARLIER APPLICATION NUMBER: 60/079,624

EARLIER FILING DATE: 1998-03-27

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 1820

TYPE: DNA

ORGANISM: Vargula cypridina

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1664)

FEATURE:

OTHER INFORMATION: Vargula (cypridina) Luciferase

PUBLICATION INFORMATION:

PATENT DOCUMENT NUMBER: JP 3-30678

PATENT FILING DATE: 1989-06-29

PUBLICATION DATE: 1991-02-08

PUBLICATION INFORMATION:

AUTHORS: Thompson, E.M.

TITLE: Cloning and expression of cDNA for the luciferase from the marine

JOURNAL: Proc. Natl. Acad. Sci. USA

VOLUME: 86(17)

PAGES: 1326-1332

DATE: 1989-09

US-09-277-716-4

Query Match 79.0%; Score 15.8; DB 4; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGCTT 19
|||||
Db 1719 TTCTTTTATCTTCGCT 1701

RESULT 10
US-08-597-274A-4/c

Sequence 4, Application US/08597274A

Patent No. 6247995

GENERAL INFORMATION:

APPLICANT: Bryan, Bruce

TITLE OF INVENTION: BIOLUMINESCENT NOVELTY ITEMS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/597,274A

1
FILING DATE: 02/06/96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L,
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6680-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1820 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1664
OTHER INFORMATION: Vargula (cypridina) luciferase
PUBLICATION INFORMATION:
AUTHORS: Thompson et al.
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 86
PAGES: 6567-6571
DATE: (1989)
US-08-597-274A-4
Query Match 79.0%; Score 15.8; DB 4; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 TTCTTTTATCTTCGCTT 19
DB 1719 TTCTTTTATCTTCGCT 1701
RESULT 11
US-08-908-909-4/C
Sequence 4, Application US/08908909
Patent No. 6416960
GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
TITLE OF INVENTION: DETECTION AND VISUALIZATION OF
TITLE OF INVENTION: NEOPLASTIC TISSUES AND OTHER TISSUES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,909
FILING DATE: 08-Aug-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/023,374
FILING DATE: 08-Aug-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L,
REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6680-108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1820 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1664
OTHER INFORMATION: Vargula (cypridina) luciferase
PUBLICATION INFORMATION:
AUTHORS: Thompson et al.
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 86
PAGES: 1326-1332
DATE: (1989)
US-08-908-909-4
DOCUMENT NUMBER: JP 3-30678 Osaka (Tsuji)
Query Match 79.0%; Score 15.8; DB 4; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 TTCTTTTATCTTCGCTT 19
DB 1719 TTCTTTTATCTTCGCT 1701
RESULT 12
US-09-609-161B-4/C
Sequence 4, Application US/09609161B
Patent No. 6436682
GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS,
FILE REFERENCE: 24729-121B
CURRENT APPLICATION NUMBER: US/09/609,161B
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/277,716
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/102,939
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/089,367
PRIOR FILING DATE: 1998-06-15
PRIOR APPLICATION NUMBER: 60/079,624
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 4
LENGTH: 1820
TYPE: DNA
ORGANISM: Vargula cypridina
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1664)
OTHER INFORMATION: Vargula (cypridina) luciferase
PUBLICATION INFORMATION:
PATENT DOCUMENT NUMBER: JP 89167689
PATENT FILING DATE: 1989-06-29
PUBLICATION DATE: 1991-02-08
PUBLICATION INFORMATION:
AUTHORS: Thompson, E.M.
AUTHORS: Nagata, S.

AUTHORS: Tsuji, F.I.
TITLE: Cloning and expression of cDNA for the luciferase from the marine
JOURNAL: Proc. Natl. Acad. Sci. USA
VOLUME: 86(17)
PAGES: 1326-1332
DATE: 1989-09
US-09-609-161B-4

Query Match 79.0%; Score 15.8; DB 4; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCTTTTATCTTCGCT 19
|||||
Db 1719 TCTTTTATCTTCGCT 1701

RESULT 13
US-08-990-103-4/c

Sequence 4, Application US/08990103
Patent No. 6458547

GENERAL INFORMATION:

APPLICANT: Bruce J. Bryan
APPLICANT: Stephen Gaalena

APPLICANT: Randall B. Murphy

TITLE OF INVENTION: APPARATUS AND METHOD FOR DETECTING AND
NUMBER OF INVENTION: IDENTIFYING INFECTIOUS AGENTS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE:

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/990,103

FILING DATE: 12-DEC-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/037,675,

FILING DATE: 02-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/033,745

FILING DATE: 12-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6680-112

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1820 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1...1664

OTHER INFORMATION: Vargula (Cypridina) Luciferase

PUBLICATION INFORMATION:

AUTHORS: Thompson et al.

JOURNAL: Proc. Natl. Acad. Sci. U.S.A.

VOLUME: 86
PAGES: 1326-1332
DATE: (1989)
DOCUMENT NUMBER: JP 3-30678 Osaka (Tsuji)
US-08-990-103-4

Query Match 79.0%; Score 15.8; DB 4; Length 1820;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCTTTTATCTTCGCT 19
|||||
Db 1719 TCTTTTATCTTCGCT 1701

RESULT 14

US-08-003-311B-1/c

Sequence 1, Application US/0800311B

Patent No. 544166

GENERAL INFORMATION:

APPLICANT: Ecker, Joseph R.

APPLICANT: Kiebert, Joseph J.

TITLE OF INVENTION: Constitutive Triple Response Gene

NUMBER OF INVENTION: and Mutations

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/003,311B

FILING DATE: January 12, 1993

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/928,464

FILING DATE: August 10, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Lori Y. Beardsell

REGISTRATION NUMBER: 34,293

REFERENCE/DOCKET NUMBER: UPN-1108

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3439

TELEFAX: 215-568-3100

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3033 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 118..2583

US-08-003-311B-1

Query Match 79.0%; Score 15.8; DB 1; Length 3033;

Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCTTTTATCTTCGCTA 20
|||||
Db 3011 TCTTTTATCTTCGCTA 2993

RESULT 15
US-08-261-432-1/C
Sequence 1, Application US/08261432
Patent No. 5602322
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5602322ris
STREET: One Liberty Place - 46th Floor
City: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,432
FILING DATE: June 17, 1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE//DOCKET NUMBER: UPN-1864
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 118..2583
US-08-261-432-1

Query Match 79.0%; Score 15.8; DB 1; Length 3033;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Caps 0;

OY 2 TCTTTTATCTCGGTTA 20
||||||| ||||| ||
Db 3011 TCTTTTACCTCGCTTA 2993

Search completed: December 10, 2002, 22:54:42
Job time : 34.3876 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 : Search time 25.9218 Seconds
(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-23
Perfect score: 20
Sequence: 1 tctcttttatcttcggtta 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*
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11: /cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	US-09-865-579A-13	Sequence 13, Appl
2	20	100.0	20	US-09-865-579A-23	Sequence 23, Appl
3	20	100.0	2007	US-09-452-599-169	Sequence 169, App
4	17.4	87.0	910	US-09-974-300-1089	Sequence 1089, Ap
5	17.4	87.0	1911	US-09-938-842A-3533	Sequence 3533, Ap
6	16.8	84.0	1641	US-09-070-927A-582	Sequence 582, App
7	16.8	84.0	173808	US-10-003-806-10	Sequence 10, Appl
8	16.4	82.0	2000	US-09-938-842A-4201	Sequence 4201, Ap
9	16.4	82.0	147309	US-09-742-312-3	Sequence 3, Appl
10	15.8	79.0	140	US-09-910-430-21	Sequence 21, Appl
11	15.8	79.0	323	US-09-878-574-4955	Sequence 4555, Ap
12	15.8	79.0	516	US-09-728-444-1101	Sequence 1101, Ap
13	15.8	79.0	1119	US-09-815-242-7059	Sequence 7059, Ap
14	15.8	79.0	1820	US-09-803-211-4	Sequence 4, Appl
15	15.8	79.0	1820	US-09-746-485A-4	Sequence 4, Appl
16	15.8	79.0	2468	US-09-925-301-293	Sequence 293, App
17	15.8	79.0	5630	US-09-871-388-1	Sequence 1, Appl
18	15.8	79.0	6560	US-09-808-602-76	Sequence 76, Appl
19	15.8	79.0	9729	US-09-808-602-12	Sequence 12, Appl

C 20	15.8	79.0	9826	9	US-09-808-602-7	Sequence 7, Appl
C 21	15.8	79.0	12566	10	US-09-764-869-2035	Sequence 2035, Ap
C 22	15.4	77.0	1099	10	US-09-925-300-736	Sequence 736, App
C 23	15.4	77.0	1626	10	US-09-119-855-6	Sequence 6, Appl
C 24	15.4	77.0	2000	10	US-09-887-576-128	Sequence 128, App
C 25	15.4	77.0	2694	10	US-09-119-855-4	Sequence 4, Appl
C 26	15.4	77.0	3977	10	US-09-801-574-33	Sequence 33, Appl
C 27	15.4	77.0	9919	12	US-10-079-035-1	Sequence 1, Appl
C 28	15.2	76.0	116	10	US-09-815-242-723	Sequence 723, App
C 29	15.2	76.0	129	10	US-09-815-242-408	Sequence 408, App
C 30	15.2	76.0	216	10	US-09-983-965-2187	Sequence 2187, Ap
C 31	15.2	76.0	239	10	US-09-983-965-4010	Sequence 4010, Ap
C 32	15.2	76.0	267	10	US-09-815-242-3863	Sequence 3863, Ap
C 33	15.2	76.0	284	10	US-09-815-242-275	Sequence 275, App
C 34	15.2	76.0	289	10	US-09-815-242-156	Sequence 156, App
C 35	15.2	76.0	291	10	US-09-815-242-6454	Sequence 6454, Ap
C 36	15.2	76.0	309	10	US-09-815-242-265	Sequence 265, App
C 37	15.2	76.0	382	10	US-09-864-761-206	Sequence 206, App
C 38	15.2	76.0	385	10	US-09-960-352-8405	Sequence 8405, App
C 39	15.2	76.0	411	10	US-09-964-824A-205	Sequence 205, App
C 40	15.2	76.0	418	10	US-09-960-352-4845	Sequence 4845, App
C 41	15.2	76.0	529	10	US-09-983-965-2109	Sequence 2109, App
C 42	15.2	76.0	585	10	US-09-864-761-15399	Sequence 15399, A
C 43	15.2	76.0	670	10	US-09-867-550-903	Sequence 903, App
C 44	15.2	76.0	774	9	US-09-870-759-15	Sequence 15, Appl
C 45	15.2	76.0	867	10	US-09-974-300-6287	Sequence 6287, Ap

ALIGNMENTS

RESULT 1
US-09-865-579A-13
; Sequence 13, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865, 579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to meca gene
US-09-865-579A-13
Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTTTTATCTTCGCTTA 20
DB 1 TCTTTTATCTTCGCTTA 20
RESULT 2
US-09-865-579A-23
; Sequence 23, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:


```
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
; FILE REFERENCE: 958-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-865-579A-23
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Query Match          100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 TTCTTTTATCTCGGTTA 20
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Db 1 TTCTTTTATCTCGGTTA 20
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RESULT 3
US-09-452-599-169/c
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: To Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169
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Query Match          100.0%; Score 20; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 TTCTTTTATCTCGGTTA 20
    |||
Db 1167 TTCTTTTATCTCGGTTA 1148
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RESULT 4
US-09-974-300-1089/c
; Sequence 1089, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
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; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085,500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1089
; LENGTH: 910
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-1089
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Query Match          87.0%; Score 17.4; DB 10; Length 910;
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 TTCTTTTATCTCGGTT 19
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Db 552 TCCTTTTATCTCGGTT 534
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RESULT 5
US-09-938-842A-3533/c
; Sequence 3533, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMB: : US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3533
; LENGTH: 1911
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3533
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Query Match          87.0%; Score 17.4; DB 9; Length 1911;
Best Local Similarity 94.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 TTCTTTTATCTCGGTT 19
    |||
Db 219 TTCATTTTATCTCGGTT 201
```

```
RESULT 6
US-09-070-927A-582/c
; Sequence 582, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
; APPLICANT: Patrick J. Dillon
; APPLICANT: Steven Barash
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
```

```

CORRESPONDENCE ADDRESS:
ADDRESSSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14

ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: P8369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 582:
SEQUENCE CHARACTERISTICS:
LENGTH: 1641 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 582:

US-09-070-927A-582

Query Match      84.0%; Score 16.8; DB 10; Length 1641;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTCTTTTATCTTCGGTTA 20
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DB      1581 TTCTTTTATCTTCGGTTA 1562

RESULT 7
US-10-003-806-10/c
Sequence 10, Application US/10003806
Patent No. US2002011929A1
GENERAL INFORMATION:
APPLICANT: Bishop, Colin E.
APPLICANT: Agouluk, Alexander I.
APPLICANT: Zhu, Qichao
TITLE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY
FILE REFERENCE: P020606US/10024824
CURRENT APPLICATION NUMBER: US/10/003,806
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 60/245,872
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 173808
TYPE: DNA
ORGANISM: Mouse
US-10-003-806-10

Query Match      84.0%; Score 16.8; DB 12; Length 173808;
Best Local Similarity 90.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 TTCTTTTATCTTCGGTTA 20
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DB      140864 TTCTTTTATCTTCGGTTA 140845

RESULT 8
US-09-938-842A-4201
Sequence 4201, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Krieps, Joel
APPLICANT: Mang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4201
LENGTH: 2000
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-4201

Query Match      82.0%; Score 16.4; DB 9; Length 2000;
Best Local Similarity 94.4%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTCTTTTATCTTCGGT 18
        ||||| ||||| ||||| |||
DB      1919 TTCTTTTATCTTCGGT 1936

RESULT 9
US-09-742-312-3/c
Sequence 3, Application US/09742312
Patent No. US20020045166A1
GENERAL INFORMATION:
APPLICANT: CHANDRAMOULISARAN, Ishwar et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00838
CURRENT APPLICATION NUMBER: US/09/742,312
CURRENT FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 147309
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1) --(147309)
OTHER INFORMATION: n = A,T,C or G
US-09-742-312-3

Query Match      82.0%; Score 16.4; DB 10; Length 147309;
Best Local Similarity 94.4%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TCTTTTATCTTCGGTT 19
        ||||| ||||| ||||| |||
DB      93310 TCTTTTATCTTCGGTT 93293
```

```
RESULT 10
US-09-910-430-21
; Sequence 21, Application US/09910430
; Patent No. US2002012735A1
; GENERAL INFORMATION:
; APPLICANT: Godfroi, Edmond
; APPLICANT: Bollen, Alex
; APPLICANT: Lebouille, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANM229.001CPI
; CURRENT APPLICATION NUMBER: US/09/910,430
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 140
; TYPE: DNA
; ORGANISM: Ixodes ricinus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3)
; OTHER INFORMATION: A,C,T or G
; NAME/KEY: unsure
; LOCATION: (10)
; OTHER INFORMATION: A,C,T or G
; NAME/KEY: unsure
; LOCATION: (30)
; OTHER INFORMATION: A,C,T or G
US-09-910-430-21

Query Match          79.0%; Score 15.8; DB 10; Length 140;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TTCTTTTATCTTCGGTT 19
    |||||  |||||
Db 54 TTCTTTTATCTTCGGTT 72

RESULT 11
US-09-878-574-4955
; Sequence 4955, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 4955
; LENGTH: 323
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-005-Q1-B1-B4
US-09-878-574-4955

Query Match          79.0%; Score 15.8; DB 10; Length 323;
Best Local Similarity 89.5%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 2 TTCTTTTATCTTCGGTTA 20
    |||||  |||||
Db 170 TTCTTTTATCTTCGGTTA 188

RESULT 12
US-09-728-444-1101/C
; Sequence 1101, Application US/09728444
; Patent No. US20020161207A1
; GENERAL INFORMATION:
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020161207A1 Murine Polynucleotide Sequences
; TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
; FILE REFERENCE: LEX-0100-USA
; CURRENT APPLICATION NUMBER: US/09/728,444
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,360
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 1206
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1101
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(516)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-444-1101

Query Match          79.0%; Score 15.8; DB 9; Length 516;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TTCTTTTATCTTCGGTT 19
    |||||  |||||
Db 299 TTCTTTTATCTTCGATT 281

RESULT 13
US-09-815-242-7059/C
; Sequence 7059, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA-011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
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; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7059
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1119)
US-09-815-242-7059

Query Match          79.0%; Score 15.8; DB 10; Length 1119;
Best Local Similarity 89.5%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTCCTTTTATCTCGGTT 19
Db      681 TTCCTTTTATATCTGCTT 663

RESULT 14
US-09-803-211-4/C
; Sequence 4, Application US/09803211
; Patent No. US20020004942A1
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAnuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: 08/09/803,211
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/444,762
; FILING DATE: 11-22-99
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/757,046
; FILING DATE: 11-25-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/597,274
; FILING DATE: 02-06-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24727-105F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-450-8499
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1664
; OTHER INFORMATION: Vargula (cypridina) luciferase
```

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; PUBLICATION INFORMATION:
; AUTHORS: Thompson et al.
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
; VOLUME: 86
; PAGES: 1326-1332
; DATE: (1989)
; DOCUMENT NUMBER: JP 3-30678 Osaka (Tsuji)
US-09-803-211-4

Query Match          79.0%; Score 15.8; DB 10; Length 1820;
Best Local Similarity 89.5%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTCCTTTTATCTCGGTT 19
Db      1719 TTCCTTTTATCTGCTT 1701

RESULT 15
US-09-746-485A-4/C
; Sequence 4, Application US/09746485A
; Patent No. US20020090659A1
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; TITLE OF INVENTION: DETECTION AND VISUALIZATION OF NEOPLASTIC
; TISSUES AND OTHER TISSUES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAnuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,485A
; FILING DATE: 22-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/908,909
; FILING DATE: 08-AUG-1997
; APPLICATION NUMBER: 60/023,374
; FILING DATE: 08-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24729-108B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8403
; TELEFAX: 858-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1664
; OTHER INFORMATION: Vargula (cypridina) luciferase
; PUBLICATION INFORMATION:
; AUTHORS: Thompson et al.
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
; VOLUME: 86
; PAGES: 1326-1332
; DATE: (1989)
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DOCUMENT NUMBER: JP 3-30678 Osaka (Tsuji)
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-746-485A-4

Query Match 79.0%; Score 15.8; DB 10; Length 1820;
Best Local Similarity 89.5%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTT 19
|||||
DB 1719 TTCTTTTATCTTCGGCT 1701

Search completed: December 11, 2002, 06:10:07
Job time : 75.9218 secs

Email: acameron@caltech.edu
Plate: 73 row: G column: 7

Seq primer: 17
Class: BAC ends

High quality sequence stop: 534.

Location/Qualifiers

FEATURES

source

1. 534
/organism="Strongylocentrotus purpuratus"

/db_xref="taxon:7668"

/clone="Plate-73 Col-7 Row-G"

/clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"

/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli DH10B"

BASE COUNT 162 a 108 c 76 g 177 t 11 others

ORIGIN

Query Match 92.0%; Score 18.4; DB 17; Length 534;
Best Local Similarity 95.0%; Pred. No. 9.5e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 TTCTTTTATCTTCGCTTA 20
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Db 443 TTCTTTTATCTTCGCTTA 462

RESULT 2
B1180052/c 676 bp mRNA linear EST 09-JUL-2001
LOCUS EST520997 CSTE Solanum tuberosum cDNA clone CSTE21B11 5' sequence.

DEFINITION mRNA sequence.
B1180052
B1180052.1 GI:14645863

KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 676)

van der Hoeven, R., Bezzerides, J., Bachem, C., Visser, R., Cho, J.,
Chieningo, A., Bougrl, O., Buell, C.R., Konning, C., Tanksley, S. and
Baker, B.

Generation of ESTs from in vitro grown microtubers

Contact: Cathy Romning

The Institute for Genomic Research

For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com

Seq primer: MJ3F-R.
Location/Qualifiers

1. 676
/organism="Solanum tuberosum"

/cultivar="BinTje"

/db_xref="taxon:4113"

/clone="CSTE21B11"

/clone_lib="CSTE"

/tissue.type="axillary buds of stem explants; growing
sink-tubers"

/dev_stage="7, 8 and 10 days"

/lab_host="SOLR"

/note="Vector: Bluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, Wageningen
University, The Netherlands). The cDNA libraries will
attempt to capture the induction and initiation/initial
growth of the tuber in an in vitro system as described in
Bachem et al. (Plant Journal, 1996). Small microtubers
developed from axillary buds attached to stem explants when
placed on a high sucrose medium (10%). Visible
morphological changes occur synchronously at day five in
the axillary buds. The first library, cSTA (1-20) consists
of axillary buds harvested on days 1-3. This targets

those genes involved in induction of the microtubers. The
following libraries, cSTA (21-40) and cSTA (41-60),
capture genes involved in tuber initiation and outgrowth.
This library is noted as p3 in Tanksley lab notebooks."

BASE COUNT 245 a 123 c 111 g 197 t

ORIGIN

Query Match 92.0%; Score 18.4; DB 13; Length 676;
Best Local Similarity 95.0%; Pred. No. 8.7e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 TTCTTTTATCTTCGCTTA 20
||||||| |||||||
Db 82 TTCTTTTATCTTCGCTTA 63

RESULT 3
B1179988/c 725 bp mRNA linear EST 09-JUL-2001
LOCUS EST520933 CSTE Solanum tuberosum cDNA clone CSTE21A12 5' sequence.
DEFINITION mRNA sequence.
B1179988
B1179988.1 GI:14645799

KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 725)

van der Hoeven, R., Bezzerides, J., Bachem, C., Visser, R., Cho, J.,
Chieningo, A., Bougrl, O., Buell, C.R., Konning, C., Tanksley, S. and
Baker, B.

Generation of ESTs from in vitro grown microtubers

Contact: Cathy Romning

The Institute for Genomic Research

For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com

Seq primer: MJ3F-R.
Location/Qualifiers

1. 725
/organism="Solanum tuberosum"

/cultivar="BinTje"

/db_xref="taxon:4113"

/clone="CSTE21A12"

/clone_lib="CSTE"

/tissue.type="axillary buds of stem explants; growing
sink-tubers"

/dev_stage="7, 8 and 10 days"

/lab_host="SOLR"

/note="Vector: Bluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, Wageningen
University, The Netherlands). The cDNA libraries will
attempt to capture the induction and initiation/initial
growth of the tuber in an in vitro system as described in
Bachem et al. (Plant Journal, 1996). Small microtubers
developed from axillary buds attached to stem explants when
placed on a high sucrose medium (10%). Visible
morphological changes occur synchronously at day five in
the axillary buds. The first library, cSTA (1-20) consists
of axillary buds harvested on days 1-3. This targets
those genes involved in induction of the microtubers. The
following libraries, cSTA (21-40) and cSTA (41-60),
capture genes involved in tuber initiation and outgrowth.
This library is noted as p3 in Tanksley lab notebooks."

BASE COUNT 257 a 137 c 120 g 211 t

ORIGIN

Query Match 92.0%; Score 18.4; DB 13; Length 725;
Best Local Similarity 95.0%; Pred. No. 8.4e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY	1	TTCCTTTTATCCTTGCGTTA	20
Db	82	TTCCTTTTATCCTTGCGTTA	63
RESULT 4			
H1436018/c	B1436018	822 bp	mRNA
LOCUS	EST53879 cstd	Solanum tuberosum	cDNA clone cSTD2IA12 5' sequence,
DEFINITION	mRNA sequence.		
ACCESSION	B1436018		
VERSION	B1436018.1	GI:15260708	
KEYWORDS	EST.		
SOURCE	Potato.		
ORGANISM	Solanum tuberosum		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;		
	Asteridae; euasteroids I; Solanales; Solanaceae; Solanum.		
	1 (bases 1 to 822)		
REFERENCE	van de Hoeven,R., Bezzerides,J., Ewing,E., Cho,J., Chiemlingo,A.,		
AUTHORS	Bongiri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.		
TITLE	Generations of ESTs from dormant potato tubers		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Cathy Ronning The Institute for Genomic Research For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdnaresgen.com Seq primer: M13F-R.		
FEATURES			
source	Location/Qualifiers		
	1..822		
	/organism="Solanum tuberosum"		
	/cultivar="Kennebec"		
	/db_xref="taxon:4113"		
	/clone="cSTD2IA12"		
	/clone_1fb="GSVD"		
	/tissue_type="dormant tuber"		
	/dev_stage="one month post-harvest"		
	/lab_host="SOLR"		
	/note="Vector: pBluescript SK(-); Site1: EcoRI; Site2:		
	XhoI; This library targets genes expressed in dormant		
	tubers. This library was made from sections of dormant		
	tuber, avoiding the buds and epidermis. Tubers were stored		
	for one month post-harvest at 40C. The tuber was peeled,		
	well away from the surface. Then it was chopped into 1-2		
	mm cubes and immediately frozen in liquid nitrogen. This		
	library is noted as P4 in Tanksley lab notebooks."		
BASE COUNT	280 a	151 c	150 g
ORIGIN			241 t
Query Match	92.0%, Score 18.4; DB 13; Length 822;		
Best Local Similarity	95.0%; Pred. NO. Be+03;		
Matches	19; Conservative	0; Mismatches	1; Indels
	0; Gaps	0;	
Oy	1	TTCCTTTTATCCTTGCGTTA	20
Db	82	TTCCTTTTATCCTTGCGTTA	63
RESULT 5			
H8301848	B8301848	294 bp	mRNA
LOCUS	B8301848 RIKEN full-length enriched, adult male corpora		
DEFINITION	quadrigenina Mus musculus cDNA clone B23003M19 3', mRNA sequence.		
ACCESSION	B8301848		
VERSION	B8301848.1	GI:9002553	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	1 (bases 1 to 294)		
REFERENCE	Kono,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci		

P., Endo, T., Fukuda, S., Fukuinishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horii, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyoosawa, H., Kojima, Y., Kondo, S., Koyama, S., Kuwahara, C., Kusakabe, M., Matsuyama, A., Miki, R., Mizuno, I., Nakamura, M., Oda, H., Okazaki, I., Ono, T., Owai, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamada, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Kono, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suwhito-cho,
Tel.: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Nishiyama, Y., Wetlewer, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotabilization and thermocycling of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Katsunami, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

Location/Qualifiers
1. 294
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="B230033M19"
/clone_lib="RIKEN full-length enriched, adult male corpora quadrigenina"
/sex="male"
/tissue_type="corpora quadrigenina"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGGAGGAGGATCCACGACCTTTTGTTCCTTTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGGAGGAGGATCCGATTAAATTAATTCGCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda PLC I.

BASE COUNT 65 a 57 g 110 t
ORIGIN

Query Match 87.0%: Score 17.4; DB 10; Length 294;
Best Local Similarity 94.7%: Pred. No. 2.5e+04;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTCTTTTTTACTTCGGTTT 19

8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."

BASE COUNT

167 a 39 c 44 g 169 t

Query Match

87.0%: Score 17.4; DB 14; Length 419;

Best Local Similarity 94.7%: Pred. No. 2.2e+04;

Matches 18: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TCTTTTATCTTCGCTTA 20

Db 289 TCTTTTATCTTCGCTTA 271

RESULT 8

LOCUS HO596612/c 428 bp mRNA linear EST 24-JUN-2002

DEFINITION P1ESTOab20b10.y1 Plasmodium falciparum 3D7 asexual cDNA Plasmodium

HO596612 falciparum cDNA 5', mRNA sequence.

KEYWORDS EST. HO596612.1 GI:21543338

SOURCE

Plasmodium falciparum. malarial parasite P. falciparum. Plasmodium falciparum Eukaryota: Alveolata: Apicomplexa: Haemosporida: Plasmodium. 1 (bases 1 to 428)

REFERENCE

AUTHORS

Tang, K., Cole, R., Chakrabarti, D., Haywood, R., Clifton, S., Pape, D., Barra, M., Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Tsagarelis, V., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I., Tsagarelis, V., Richey, J., Wadkins, J., Franklin, C., Carr, L., Grow, A., Maguire, L., Richey, J., Wadkins, J., Kennedy, S., Levins, D., Watson, R., Wilson, R. and Sibley, D.

TITLE

JOURNAL

COMMENT

Unpublished (2001)
WashU Plasmodium EST Project
Contact: L. David Sibley
WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: L. David Sibley (sibley@borcim.wustl.edu), Washington University
Seq primer: -400p from Gibco.

FEATURES

source

1..428
Location/Qualifiers
/organism="Plasmodium falciparum"
/db_xref="taxon:5833"
/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2: XhoI; Library was constructed by Debopam Chakrabarti. Total RNA samples were isolated from mixed stage zygonts (0.1%)-lysed P. falciparum 3D7 infected erythrocytes by the acidic guanidium-phenol chloroform method. The poly A+ RNA was isolated by the polyAT-tract mRNA isolation system (Promega, WI) using streptavidin Magnosphere particles. Directional cDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of 1 ZapII vector using the Zap cDNA synthesis kit (Stratagene, CA). The average size of the cDNA inserts in the library was between 1.0 and 1.5kb. Clones were mass excised using the Exassist helper phage (Stratagene), the phagemids were precipitated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."

BASE COUNT

169 a 39 c 44 g 176 t

Query Match

87.0%: Score 17.4; DB 14; Length 428;

Best Local Similarity 94.7%: Pred. No. 2.1e+04;

Matches 18: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TCTTTTATCTTCGCTTA 20

Db 289 TCTTTTATCTTCGCTTA 271

RESULT 9

LOCUS BU031040 477 bp mRNA linear EST 23-AUG-2002

DEFINITION OHJ17D20.y9.ab1 OH_EFGHJ sunflower RHA280 Helianthus annuus cDNA

clone OHJ17D20, mRNA sequence.

ACCESSION BU031040

VERSION BU031040.1 GI:22466560

KEYWORDS EST.

SOURCE

Common sunflower.
Helianthus annuus
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Asteridae: easterids II: Asterales: Asteraceae: Asteroideae: Heliantheae: Helianthus.
1 (bases 1 to 477)

REFERENCE

AUTHORS

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Riesberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://comgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
Belongs to contig OH_CA.Contig194465, see http://cgpdb.ucdavis.edu/ for details.
Plate: OHJ17 row: D column: 20.

FEATURES

source

1..477
Location/Qualifiers
/organism="Helianthus annuus"
/cultivar="RHA280"
/db_xref="taxon:4232"
/clone_lib="OHJ17D20"
/clone_1ib="OH_EFGHJ sunflower RHA280"
/lab_host="E.coli"
/note="Vector: pBRCDNA51AB: The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=OH_EFGHJ sunflower RHA280
TAG_TISSUE=flowers environmental stress
TAG_SEQ=CGAATGCGC"

BASE COUNT

167 a 76 c 80 g 154 t

Query Match

87.0%: Score 17.4; DB 14; Length 477;

Best Local Similarity 94.7%: Pred. No. 2e+04; 1; Indels 0; Gaps 0;

Matches 18: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TCTTTTATCTTCGCTTA 20

Db 197 TCTTTTATCTTCGCTTA 215

RESULT 10

AW622642

LOCUS AM622642 543 bp mRNA linear EST 18-MAY-2001
 DEFINITION EST313442 tomato root during/after fruit set, Cornell University
 ACCESSION Lycopersicon esculentum cDNA clone CLEX15012 5', mRNA sequence.
 VERSION AM622642
 KEYWORDS EST, GI:7334289
 SOURCE
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
 REFERENCE 1 (bases 1 to 543)
 AUTHORS van der Hoeven, R.S., Garvin, D., Matern, A.L., Holt, I.E., Kochian, L., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Romling, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
 TITLE Generation of ESTs from tomato root, during and after fruit set
 JOURNAL Unpublished (1999)
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.
 FEATURES
 source
 1..543
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="CLEX15012"
 /clone_lib="tomato root during/after fruit set, Cornell University"
 /issue_type="root"
 /dev_stage="plants during and after fruit-set"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850)."
 BASE COUNT 145 a 107 c 92 g 199 t
 ORIGIN
 Query Match 87.0%; Score 17.4; DB 10; Length 543;
 Best Local Similarity 94.7%; Pred. No. 1.9e+04;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TCTTTTATCTTCGCTTA 20
 |||||||||||||
 Db 171 TCTTTTATCTTCGCTTA 189
 :SULT 11
 :A195C01P 548 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 195c01, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL477924
 VERSION AL477924.1 GI:11841736
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 REFERENCE 1 (bases 1 to 548)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and miles@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 details of T. brucei sequencing at the Sanger Centre are available at <http://www.sanger.ac.uk/Projects/T-brucei/>.
 FEATURES
 source
 1..548
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="195c01"
 /clone_lib="195c01"
 BASE COUNT 158 a 130 c 43 g 217 t
 ORIGIN
 Query Match 87.0%; Score 17.4; DB 17; Length 548;
 Best Local Similarity 94.7%; Pred. No. 1.9e+04;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTCTTTTATCTTCGCTT 19
 |||||||||||||
 Db 8 TTCTTTTATCTTCGCTT 26
 RESULT 12
 LOCUS B1509735/c 552 bp mRNA linear EST 08-APR-2002
 DEFINITION BBI70019A10C12.5 Bee Brain Normalized/Subtracted Library, BBI7 Apis mellifera cDNA clone BBI70019A10C12 5', mRNA sequence.
 ACCESSION B1509735
 VERSION B1509735.1 GI:15360109
 KEYWORDS EST.
 SOURCE honeybee.
 ORGANISM Apis mellifera
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoecrita; Aculeata; Apoidea; Apidae; Apis.
 REFERENCE 1 (bases 1 to 552)
 AUTHORS Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L., Pardinas, J., Robertson, H.M., Soares, R. and Robinson, G.E.
 TITLE Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee
 JOURNAL Genome Res. 12 (4), 555-566 (2002)
 MEDLINE 21929762
 COMMENT Contact: Gene E. Robinson
 Department of Entomology
 University of Illinois
 505 S. Goodwin Ave., Urbana, IL 61801, USA
 Tel: 217 265 0309
 Fax: 217 244 3499
 Email: gene@life.uiuc.edu
 This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
 REPEAT IN THE SEQUENCE
 Simple repeat STRAND (+) ELEMENT (ATC)n LOCATION [39,63].
 PCR Primers
 FORWARD: TATACGCTCACTATAGG
 BACKWARD: ATTACCTCACTAAG
 Plate: BBI70019A10 row: C column: 12
 Seq primer: AGCGATACCAATTTCACAGCA
 High quality sequence stop: 552.
 FEATURES
 source
 1..552
 /organism="Apis mellifera"
 /strain="mixed strains of European bees, predominantly A.m. ligustica"
 /db_xref="taxon:7460"

```

/c/clone="BB170019A10C12"
/clone_lib="Bee Brain Normalized/Subtracted Library, BB17"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/notice="Organ: brain; Vector: pT73-Pac; Site:1; EcoRI;
Site:2; NotI; This BB17 cDNA library was generated by
subtraction of the BB16 library with 4000 previously
sequenced clones. The BB16 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups."
BASE COUNT      175 a      83 c      97 g      197 t
ORIGIN
Query Match      87.0%; Score 17.4; DB 13; Length 552;
Best Local Similarity 94.7%; Pred. No. 1.9e+04;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTCTTTTATCTCGGTT 19
Db      435 TTCTTTTATCTCGGTT 417
|||||
|||||

RESULT 13      582 bp  mRNA  linear  EST_03-SEP-1997
AA579610/c     nm79b03.s1 NCI-CGAP_C09 Homo sapiens cDNA clone IMAGE:1074413 3'
LOCUS          similar to contains Alu repetitive element;contains element MER22
DEFINITION     repetitive element ; , mRNA sequence.
ACCESSION      AA579610
VERSION        AA579610
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 582)
AUTHORS       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNALS       Unpublished (1997)
COMMENTS      Contact: Robert Strausberg, Ph.D.
              Email: cgaaps-remail.nih.gov
              Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
              , Ph.D.
              cDNA Library Preparation: M. Bento Soares, Ph.D.
              cDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/ILNI, at:
              www-bio.lnlnl.gov/bhrp/image/image.html
              Seq primer: -40m13 fwd. ET from Amersham
              High quality sequence stop: 475.
FEATURES
SOURCE
1..582
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1074413"
/clone_lib="NCI-CGAP_C09"
/tissue_type="Colon tumor RER+"
/lab_host="DH10B"
/notice="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
RER+ colon tumor, and was then primed with a Not I -
oligo(47) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo (Soares4

```

```

}
BASE COUNT      207 a      115 c      122 g      138 t
ORIGIN
Query Match      87.0%; Score 17.4; DB 9; Length 582;
Best Local Similarity 94.7%; Pred. No. 1.9e+04;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTCTTTTATCTCGGTT 19
Db      466 TTCTTTTATCTCGGTT 448
|||||
|||||

RESULT 14      582 bp  DNA  linear  GSS_02-OCT-2000
AZ369836/c     1M0120C09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
LOCUS          clone UUGC1M0120C09 R, DNA sequence.
DEFINITION     AZ369836
ACCESSION      AZ369836
VERSION        AZ369836.1 GI:10483536
KEYWORDS       GSS.
SOURCE         house mouse.
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE      1 (bases 1 to 582)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLES        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNALS       Unpublished (2000)
COMMENTS      Contact: Robert B. Weiss
              University of Utah
              University of Utah Genome Center
              Rm.308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunne@genetics.utah.edu
              Insert length: 10000 Std Error: 0.00
              Plate: 0120 row: c column: 09
              Seq primer: CACACAGCAACACCTATGACC
              Class: plasmid ends
              High quality sequence stop: 582.
FEATURES
SOURCE
1..582
/organism="Mus musculus"
/strain="C57Bl/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0120C09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notice="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57Bl/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydronically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g11473114|g11473114|g11473114|g11473114), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

```

BASE COUNT 160 a 126 c 108 g 188 t and selected for ampicillin resistance." ORIGIN

Query Match 87.0%; Score 17.4; DB 17; Length 582;
Best Local Similarity 94.7%; Pred. No. 1.9e+04;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTTATCTTCGGTT 19
|||||
Db 214 TTTCTTTTATCTTCGGTT 196

RESULT 15 617 bp DNA linear GSS 20-FEB-2001
AZ810395/C 2M0074F22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

LOCUS 2M0074F22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION

ACCESSION AZ810395
VERSION AZ810395
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 617)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meen,J.E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tinge,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0074 row: F column: 22
Seq primer: CACACACGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 617.

FEATURES
source Location/Qualifiers
1..617
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0074F22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g11473211419b/AF12972.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

BASE COUNT 174 a 127 c 159 g 157 t and selected for ampicillin resistance." ORIGIN

Query Match 87.0%; Score 17.4; DB 17; Length 617;
Best Local Similarity 94.7%; Pred. No. 1.8e+04;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTTATCTTCGGTT 19
|||||
Db 161 TTTCTTTTATCTTCGGTT 143

Search completed: December 10, 2002, 22:50:10
Job time : 1030.47 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:03:28 : Search time 91.2737 Seconds
(without alignments)
345.422 Million cell updates/sec

Title: US-09-865-579A-19
Perfect score: 14
Sequence: 1 gaagqtgtcttac 14

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	14	24	ABK85917
2	14	100.0	14	24	ABK85919
3	14	100.0	467	16	AAQ86977
4	14	100.0	1789	16	AAQ86977
5	14	100.0	2007	13	AAQ28599
6	14	100.0	2007	17	AAQ28599
7	14	100.0	2007	19	AAQ28599
8	14	100.0	2007	22	AAQ28599
9	14	100.0	2028	24	ABN92247

c	10	14	100.0	2110	14	AAQ35213	Sequence of the me
c	11	14	100.0	2322	13	AAQ25905	PP2'. Synthetic.
c	12	14	100.0	2455	16	AAQ4538	Staphylococcus aur
c	13	14	100.0	2456	22	AAH01187	Staphylococcus aur
c	14	13	92.9	301	23	AAQ39747	DNA encoding novel
c	15	13	92.9	422	22	AAK72181	Human immune/haema
c	16	13	92.9	422	22	AAK72185	Human immune/haema
c	17	13	92.9	441	22	AAK72186	Human immune/haema
c	18	13	92.9	804	24	ABN66368	Streptococcus poly
c	19	13	92.9	1065	20	AAQ82169	p. vivax Pvs28 pol
c	20	13	92.9	1377	22	AAQ85064	Mouse apoptosis me
c	21	13	92.9	1758	22	AAH56344	DNA encoding Chlam
c	22	13	92.9	1758	24	ABL92573	Chlamydia trachoma
c	23	13	92.9	2068	17	AAQ28283	A. niger Bo-1 geno
c	24	13	92.9	2826	23	AAQ74888	DNA encoding novel
c	25	13	92.9	2826	23	AAQ79117	DNA encoding novel
c	26	13	92.9	2827	23	AAQ69657	DNA encoding novel
c	27	13	92.9	5253	24	ABL92628	Chlamydia trachoma
c	28	13	92.9	5253	24	ABL92704	Chlamydia trachoma
c	29	13	92.9	5265	21	AAQ64756	C. trachomatis pmp
c	30	13	92.9	5265	22	AAH56259	Chlamydia trachoma
c	31	13	92.9	5265	24	ABL92488	Chlamydia DNA sequ
c	32	13	92.9	6735	19	AAQ52237	Streptococcus pneu
c	33	13	92.9	8766	24	ABN72581	Streptococcus agal
c	34	13	92.9	11484	22	ABAI7409	Human nervous syst
c	35	13	92.9	11484	22	ABAI7410	Human nervous syst
c	36	13	92.9	11853	22	AAQ32785	Human genomic DNA
c	37	13	92.9	14111	22	AAQ57100	DNA encoding Dros
c	38	13	92.9	14111	23	ABL10392	Drosophila melanog
c	39	13	92.9	2155561	24	ABN71557	Streptococcus poly
c	40	12.6	90.0	248	24	ABL93125	Rat metastatic tum
c	41	12.4	88.6	20	20	AAQ95153	PCR primer used to
c	42	12.4	88.6	20	20	AAQ92677	PCR primer used to
c	43	12.4	88.6	233	16	AAQ75124	E. carotovora nucle
c	44	12.4	88.6	233	23	ABV16438	Human prostate exp
c	45	12.4	88.6	275	23	ABV16229	Human prostate exp

ALIGNMENTS

RESULT 1	ABK85917	standard: DNA: 14 BP.
AC	ABK85917;	
XX		
XX		
DT	16-AUG-2002 (first entry)	
XX		
DE	Methicillin resistant Staphylococcus aureus detection primer #17.	
XX		
KW	Methicillin resistant Staphylococcus aureus; MRSA; primer: ss;	
KW	mechA; probe.	
OS	Staphylococcus aureus.	
XX		
PN	EP1160333-A2.	
XX		
PD	05-DEC-2001.	
XX		
PF	29-MAY-2001; 2001EP-0112100.	
XX		
PR	29-MAY-2000; 2000JP-0163149.	
XX		
PR	09-JUN-2000; 2000JP-0179394.	
XX		
PA	(TORJ) TOSOH CORP.	
XX		
PI	Taya T, Ishiguro T, Saito J;	
XX		
DR	WPI: 2002-395832/43.	
XX		
PT	New oligonucleotide specific for the mech methicillin-resistance gene,	
PT	useful for cleavage, detection and amplification of the gene or related	

PT mRNA -
 XX
 PS Claim 1: Page 18; 28pp; English.
 CC This invention relates to oligonucleotides used for cleaving, detecting
 CC and amplifying the meca gene (associated with methicillin resistance in
 CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
 CC a detection method employing an RNA amplification process, using RNA
 CC derived from the meca gene as template. Also disclosed is a detection
 CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
 CC amplification process in the presence of a complementary oligonucleotide
 CC probe labelled with an intercalated fluorescent dye, where complementary
 CC binding of the probe to the RNA transcription product results in a
 CC change in the fluorescent property relative to that of a situation where
 CC a complex formation is absent, and then measuring the fluorescence
 CC intensity of the reaction solution. The oligonucleotides may be used as
 CC primers or probes, for detecting methicillin-resistant *S. aureus* in
 CC clinical samples. They may also be used therapeutically to inhibit RNA
 CC reverse transcription or translation. These oligonucleotides permit
 CC rapid and very sensitive detection/identification of the meca gene, at a
 CC relatively low temperature without the need for heat denaturation of
 CC target RNA. The present sequence represents a methicillin resistant
 CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
 SQ Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 other;
 Query Match 100.0%; Score 14; DB 24; Length 14;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAGCTGTCTTAC 14
 Db 1 GAAGGTGTCTTAC 14
 RESULT 2
 ID ABK85919 standard; DNA: 14 BP.
 AC ABK85919;
 DT 16-AUG-2002 (first entry)
 DE Methicillin resistant *Staphylococcus aureus* detection primer #19.
 XX
 KW Methicillin resistant *Staphylococcus aureus*; MRSA; primer; ss;
 KM meca; probe.
 XX
 NS *Staphylococcus aureus*.
 EP1160333-AZ.
 XX
 PD 05-DEC-2001.
 XX
 PF 29-MAY-2001; 2001EP-0112100.
 XX
 PR 29-MAY-2000; 2000JP-0163149.
 XX
 PR 09-JUN-2000; 2000JP-0179394.
 XX
 PA (TOYO) TOSOH CORP.
 XX
 PI Taya T, Ishiguro T, Saito J;
 XX
 DR WPI; 2002-395832/43.
 XX
 PT New oligonucleotide specific for the meca methicillin-resistance gene,
 PT useful for cleavage, detection and amplification of the gene or related
 PT mRNA -
 XX
 PS Claim 5; Page 19; 28pp; English.
 CC
 CC This invention relates to oligonucleotides used for cleaving, detecting
 CC and amplifying the meca gene (associated with methicillin resistance in

CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
 CC a detection method employing an RNA amplification process, using RNA
 CC derived from the meca gene as template. Also disclosed is a detection
 CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
 CC amplification process in the presence of a complementary oligonucleotide
 CC probe labelled with an intercalated fluorescent dye, where complementary
 CC binding of the probe to the RNA transcription product results in a
 CC change in the fluorescent property relative to that of a situation where
 CC a complex formation is absent, and then measuring the fluorescence
 CC intensity of the reaction solution. The oligonucleotides may be used as
 CC primers or probes, for detecting methicillin-resistant *S. aureus* in
 CC clinical samples. They may also be used therapeutically to inhibit RNA
 CC reverse transcription or translation. These oligonucleotides permit
 CC rapid and very sensitive detection/identification of the meca gene, at a
 CC relatively low temperature without the need for heat denaturation of
 CC target RNA. The present sequence represents a methicillin resistant
 CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
 SQ Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 other;
 Query Match 100.0%; Score 14; DB 24; Length 14;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAGCTGTCTTAC 14
 Db 1 GAAGGTGTCTTAC 14
 RESULT 3
 ID AA086977/C
 XX
 AC AA086977 standard; DNA: 467 BP.
 DT 16-JAN-1996 (first entry)
 DE Polynucleotide probe for methicillin resistant *Staphylococcus aureus*.
 XX
 KW MRSA; methicillin resistant *Staphylococcus aureus*; probe;
 KM hybridisation; meca; MRSE; *Staphylococcus epidermidis*; ss.
 OS
 PN *Staphylococcus aureus*.
 XX
 DE4338119-AI.
 XX
 PD 11-MAY-1995.
 XX
 PF 08-NOV-1993; 93DE-4338119.
 XX
 PR 08-NOV-1993; 93DE-4338119.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Endermann R, Springer W;
 XX
 DR WPI; 1995-180108/24.
 XX
 PT Detection of methicillin resistant *Staphylococcus* - using an
 PT oligo:nucleotide derived from the meca gene
 XX
 PS Claim 2; Page 11; 14pp; German.
 XX
 CC An oligonucleotide probe having the 467 nucleotide sequence shown
 CC isolated from *S. aureus*, is capable of hybridising with the DNA or
 CC RNA of methicillin resistant *S. aureus* (MRSA). The probe is
 CC specifically derived from the meca gene of *S. aureus* and *S. epidermidis*.
 CC The meca gene product has no homology with known PBPs
 CC (penicillin-binding proteins). The new probes allow for the rapid
 CC identification of all MRSE, eradicating need for labour intensive in
 CC vitro cultivation and physiological assays.
 CC
 SQ Sequence 467 BP; 187 A; 73 C; 85 G; 122 T; 0 other;

KW Haemophilus influenzae; Moraxella catarrhalis; septicolaemia; meningitis;
KM infection; intra-abdominal infection; skin infection;
KM bacterial resistance; beta-lactam antibiotic; ds.
XX
XX Synthetic.
XX
XX WO9608582-A2.
XX
XX
XX 21-MAR-1996.
XX
XX 12-SEP-1995; 95WO-CA00528.
XX
XX 12-SEP-1994; 94US-0304732.
XX
XX (BERG/) BERGERON M G.
XX (OUEL/) OUELLETTE M.
XX (ROY/) ROY P H.
XX
XX Bergeron MG, Ouellette M, Roy PH;
XX
XX WPI: 1996-179953/18.
XX
XX
XX Method for the detection of bacterial species using probes and
XX primers - allows detection and quantification of antibiotic
XX resistant bacteria in patients, the environment and food
XX
XX
XX Claim 91; Page 144-145; 216pp; English.
XX
XX The sequences given in AAT28560-76 represent fragments derived from
XX bacterial antibiotic resistance genes which were used as probes in the
XX method of the invention for the detection of bacterial species in a
XX sample. The method of the invention comprises using probes and/or
XX amplification primers which are specific, ubiquitous and sensitive for
XX determining the presence and/or amount of nucleic acids from selected
XX bacterial species in any sample, where the bacterial nucleic acid
XX comprises a selected target region hybridisable with the probes or
XX primers. The method comprises contacting the sample with the probes
XX or primers and detecting the presence and/or amount of hybridised
XX primers or amplification products as and indication of the presence
XX and/or amount of the bacterial species. This method may be used to
XX detect commonly encountered bacterial pathogens, e.g. Escherichia coli,
XX Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis,
XX Staphylococcus pneumoniae, Staphylococcus aureus, Staphylococcus
XX epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus,
XX Streptococcus pyogenes, Haemophilus influenzae and Moraxella
XX catarrhalis. These bacterial species are associated with approx. 90% of
XX urinary tract infections and with a high percentage of other severe
XX infections including septicaemia, meningitis, pneumonia, intra-abdominal
XX infections, skin infections and other severe respiratory tract
XX infections. The method may also be used to evaluate a bacterial
XX resistance to beta- lactam antibiotics.
XX
XX
XX Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 14; DB 17; Length 2007;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 GAAGCTGTGCTTAC 14
XX |||||||||||||
XX
XX 1094 GAAGCTGTGCTTAC 1081
XX
XX
XX RESULT 7
XX AAV68337/C
XX ID AAV68337 standard; DNA; 2007 BP.
XX
XX
XX AAV68337;
XX
XX 21-JUN-1999 (first entry)
XX
XX
XX Penicillin binding protein PBP2A meca-27R gene of S. aureus 27R.
XX
XX

KW Penicillin binding protein; PBP2A-27R; meca-27R gene;
KM methicillin resistance; antibiotic; assay; purification; ss.
XX
XX Staphylococcus aureus.
XX
XX
XX EP875578-A2.
XX
XX
XX 04-NOV-1998.
XX
XX
XX 18-MAR-1992; 92EP-0302298.
XX
XX
XX 19-MAR-1991; 91US-0672704.
XX
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Blaszcak LC, Skatrud PL, Smith MC, Wu CE;
XX
XX WPI: 1998-559443/48.
XX P-PSDB: AAW81149.
XX
XX
XX New Staphylococcus aureus soluble penicillin-binding proteins and
XX their derivatives - useful for screening for compounds effective
XX against methicillin resistant organisms
XX
XX
XX Disclosure; Page 14-16; 97pp; English.
XX
XX
XX
XX This meca-27R gene encodes penicillin binding protein 2A (PBP2A-27R)
XX responsible for the methicillin resistance of Staphylococcus aureus
XX strain 27R. The invention provides new PBPs of formula SP-1-PBP2As,
XX where: SP is 0 or a signal peptide (preferably from the ampc, ompA or
XX beta-lactamase gene product); L is Met-Val or a compound of formula
XX Met-Gly-CP-(Pro)n-PBP2As, where CP = 0 or a chelating peptide (see
XX AAW81151-58) of formula (His)x-(A)y-(His)z and A-an amino acid,
XX x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above,
XX polypeptide where each monomer unit is the same or different; pro
XX is proline, n = 0 or 1; and PBP2As is soluble PBP2A-27R protein (see
XX AAW81159-62). Also claimed are polynucleotides encoding specific
XX soluble PBP2A compounds. The new PBP2A-27R proteins are useful for
XX assaying for agents useful as antibiotics against methicillin
XX resistant Staphylococcus strains by creating a kinetically inert
XX complex between a support-immobilised transition ion and a modified
XX soluble PBP2A protein comprising a chelating agent, which screens
XX for agents which bind to PBP2A proteins (disclosed). Soluble forms
XX of PBP2A-27R protein facilitate crystallisation as they lack their
XX transmembrane association region, and so are useful for x-ray
XX crystallography studies of the protein, assisting in the design of
XX antibiotic compounds against methicillin resistant Staphylococcus
XX strains (disclosed). The chelating peptide operably linked to the
XX Bp2A-27R proteins is useful for purifying PBPs.
XX
XX
XX Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 14; DB 19; Length 2007;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 GAAGCTGTGCTTAC 14
XX |||||||||||||
XX
XX 1094 GAAGCTGTGCTTAC 1081
XX
XX
XX RESULT 8
XX ABA76993/C
XX ID ABA76993 standard; DNA; 2007 BP.
XX
XX
XX ABA76993;
XX
XX 28-JAN-2002 (first entry)
XX
XX
XX Antibiotic resistance detection polynucleotide SEQ ID NO 169.
XX
XX
XX Detection; bacterial species; animal; food; environment;
XX antibiotic resistance; ds.
XX
XX

```
XX OS Unidentified.
XX PN NZ501596-A.
XX PD 29-JUN-2001.
XX PF 12-SEP-1995; 95N2-0501596.
XX PR 12-SEP-1995; 95N2-0501596.
XX PA (IDII-) IDI INFECTIO DIAGNOSTIC INC.
XX PI Bergeron MG, Ouellette M, Roy PH;
XX DR WPI: 2001-615034/71.
XX PT Method for detecting target bacterial species in a sample, comprises
XX PT detecting the presence or amount of bacterial nucleic acid amplified by
XX PT a primer derived from bacterial DNA, specific for the target bacterial
XX PT species -
XX PS
XX PS Claim 16; Page 159-160; 168pp; English.
XX CC The invention relates to detecting target bacterial species suspected to
XX CC be present in a sample, comprising contacting nucleic acids of target
XX CC bacterial species with an amplification primer pair derived from a
XX CC bacterial DNA fragment (ABA76825-ABA76861) specific for the target
XX CC bacterial species but ubiquitous for different strains, amplifying the
XX CC nucleic acid and detecting the presence or amount of an amplified
XX CC sequence as an indication of the presence or amount of the target
XX CC bacterial species. The invention includes primers and probes
XX CC (ABA76862-ABA76984) against the target bacterial species, especially
XX CC E.coli, K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae,
XX CC S.aureus, S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes,
XX CC H.influenzae, M.catarhalis and/or group A Streptococci producing
XX CC exotoxin A gene spe A, suspected to be present in a sample which is
XX CC obtained from human patients, animals, environment or food, and which
XX CC consists of one or more bacterial colonies. Oligonucleotide
XX CC probes and primers complementary to the bacterial genes encoding
XX CC resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aacB,
XX CC aacC1, aacC2, aacC3, aacA4, mecA, vanA, vanX, vanY, aacA-aphD, vat,
XX CC vga, mraA, sul and/or int (ABA76985-ABA77001) are also useful to identify
XX CC commonly encountered and clinically important resistance genes. The
XX CC invention provides a rapid method of bacterial identification that can be
XX CC achieved, which reduces the time currently required for the
XX CC identification of pathogens in the clinical laboratory.
XX CC
XX Q Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
XX
XX Query Match 100.0%; Score 14; DB 22; Length 2007;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAAGGTGTCCTTAC 14
XX DB 1094 GAAGGTGTCCTTAC 1081
XX
XX RESULT 9
XX ABN92247/c
XX ID ABN92247 standard; DNA; 2028 BP.
XX AC
XX AC ABN92247;
XX XX
XX DT 24-JUL-2002 (first entry)
XX XX
XX DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1710.
XX XX
XX KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
XX XX antibacterial; gene therapy; gene; ds.
XX XX
XX OS Staphylococcus epidermidis.
```

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XX XX US6380370-B1.
XX PN
XX PD 30-APR-2002.
XX PF 13-AUG-1998; 98US-0134001.
XX PR 14-AUG-1997; 97US-055779P.
XX PR 08-NOV-1997; 97US-064964P.
XX XX (GENO-) GENOME THERAPEUTICS CORP.
XX PA
XX PI Doucette-Stamm LA, Bush D;
XX XX
XX DR WPI: 2002-381255/41.
XX DR P-PSDB; ABP39702.
XX XX
XX PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
XX PT polypeptide, useful for diagnosing and treating bacterial infections -
XX XX
XX PS Disclosure; SEQ ID 1710; 267pp; English.
XX XX
XX CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
XX CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
XX CC given in ABP3124 to ABP37960. The S. epidermidis sequences have
XX CC antibacterial activity and can be used in gene therapy. The sequences
XX CC can also be used in the diagnosis and treatment of bacterial infections,
XX CC particularly S. epidermidis infections. The sequences can be used to
XX CC screen for compounds able to interfere with the S. epidermidis life
XX CC cycle or inhibit S. epidermidis infection.
XX CC N.B. The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from the
XX CC USPTO web site.
XX CC
XX SQ Sequence 2028 BP; 861 A; 273 C; 346 G; 547 T; 1 other;
XX
XX Query Match 100.0%; Score 14; DB 24; Length 2028;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAAGGTGTCCTTAC 14
XX DB 1115 GAAGGTGTCCTTAC 1102
XX
XX RESULT 10
XX AAQ35213/c
XX ID AAQ35213 standard; DNA; 2110 BP.
XX AC
XX AC AAQ35213;
XX XX
XX DT 06-JUN-1993 (first entry)
XX XX
XX DE Sequence of the mec A gene.
XX XX
XX KW Methicillin-resistant staphylococci; detection; primer; PCR; ss.
XX XX
XX OS Staphylococcus aureus.
XX XX
XX FH Key
XX FH Location/Qualifiers
XX FT CDS 105..2110
XX FT /*tag= a
XX XX
XX PN EP527628-A.
XX XX
XX PD 17-FEB-1993.
XX XX
XX PF 10-AUG-1992; 92EP-0307307.
XX XX
XX PR 13-AUG-1991; 91US-0744770.
XX XX
XX PA (ELIT ) LILLY & CO ELI.
XX XX
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```

PI Skatrud PL, Unal S;
XX
DR WPI; 1993-054352/07.
DR P-PSDB; AAR30845.
XX
PT Detection of methicillin-resistant staphylococci - using
PT polymerase chain reaction method, and DNA primers, for rapid,
PT sensitive and accurate detection
XX
PS Disclosure: Pages 7-10; 16pp; English.
XX
CC The inventors claim a method for detecting methicillin-resistant
CC staphylococcal infections which involves the use of the PCR primed
CC by fragments of the Staphylococcus meca gene. More specifically, the
CC initial primers used are nucleotides 141-160 and the inverse
CC complement of nucleotides 1929-1952 of the S. aureus meca gene. The
CC interlor primers are nucleotides 568-593 and the inverse complement
CC of 1647-1670 of the S. aureus meca gene.
XX
SQ Sequence 2110 BP; 896 A; 290 C; 350 G; 574 T; 0 other;

Query Match 100.0%; Score 14; DB 14; Length 2110;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGCTGCTTAC 14
DB 1198 GAAGGTGTGCTTAC 1185
|||||
|||||

RESULT 11
AAQ25905/C
ID AAQ25905 standard; DNA: 2322 BP.
XX
AC AAQ25905;
XX
XX 18-JAN-1993 (first entry)
XX
DE PBP2'.
XX
XX Polymerase chain reaction; PCR; amplification; ss.
XX
OS Synthetic.
XX
FH Key location/Qualifiers
FT misc_binding 1581..1598
FT /*tag= a
FT /label= Probe_binding_site
FT
Y JP04169200-A.
..X
PD 17-JUN-1992.
XX
PF 31-OCT-1990; 90JP-0296708.
XX
PR 31-OCT-1990; 90JP-0296708.
XX
PA (SHIO ) SHIONOGI & CO LTD.
XX
DR WPI; 1992-253403/31.
XX
PT Detection of PBP2' gene for determ. of methicillin-resistance -
PT useful esp. for detection of methicillin-resistance
PT Staphylococcus aureus
XX
PS Disclosure; Fig 1; 9pp; Japanese.
XX
CC The sequence given is the PBP2' gene. This gene could be detected
CC by the primer sequences given in AAQ25897-904. Due to the results of
CC this amplification reaction resistance to methicillin in Staphylococcus
CC aureus could be determined.
XX
SQ Sequence 2322 BP; 940 A; 324 C; 389 G; 669 T; 0 other;

```

```

Query Match 100.0%; Score 14; DB 13; Length 2322;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGCTGCTTAC 14
DB 1100 GAAGGTGTGCTTAC 1087
|||||
|||||

RESULT 12
AAT04538/C
ID AAT04538 standard; cDNA to mRNA; 2455 BP.
XX
AC AAT04538;
XX
XX 11-APR-1996 (first entry)
XX
DE Staphylococcus aureus meca protein coding sequence.
XX
XX methicillin-resistant Staphylococcus aureus; MRSA; 'meca protein;
XX antibiotic resistance; ds.
XX
OS Staphylococcus aureus.
XX
FH Key location/Qualifiers
FT CDS 134..2146
FT /*tag= a
FT /product= mec_A-pr .lein
FT
XX
XX JP07209294-A.
XX
XX 11-AUG-1995.
XX
PD 10-JAN-1994; 94JP-0012226.
XX
PE 10-JAN-1994; 94JP-0012226.
XX
XX 10-JAN-1994; 94JP-0012226.
XX
XX (DENK-) DENKA SEIKEN KK.
XX (KAWA/) KAWANO M.
XX (MITU ) MITSUBISHI CHEM CORP.
XX
DR WPI; 1995-313917/41.
DR P-PSDB; AAR80036.
XX
XX New 'mec A protein and DNA encoding it - used for the detection of
XX methicillin-resistant Staphylococcus aureus
XX
PS Example 2; Page 8-10; 15pp; Japanese.
XX
CC The present sequence codes for the mec A protein. DNA coding for
CC the 'mec A protein, which controls methicillin resistance in
CC methicillin-resistant Staph. aureus (MRSA), was obtained by PCR
CC amplification of the mec A sequence using primers AAT04537 and
CC AAT04539. The 'mec A protein (mol. wt. 40000) is useful for
CC preparation of antiserum specific for MRSA, thereby allowing
CC methicillin-resistant and methicillin-sensitive strains to be
CC distinguished.
XX
SQ Sequence 2455 BP; 997 A; 344 C; 401 G; 713 T; 0 other;

Query Match 100.0%; Score 14; DB 16; Length 2455;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGCTGCTTAC 14
DB 1233 GAAGGTGTGCTTAC 1220
|||||
|||||

RESULT 13
AAH01187/C
ID AAH01187 standard; DNA: 2456 BP.

```

XX AH01187;
 AC 24-JUL-2001 (first entry)
 XX
 DE Staphylococcus aureus nucleotide sequence SEQ ID NO:1178.
 XX
 XX Species specific; genus specific; family specific; probe; detection;
 KW identification; algal; archaeal; bacterial; fungal; parasitica;
 KW microorganism; diagnosis; translation elongation factor Tu; toxin;
 KW translation elongation factor G; RecA recombinase; resistance;
 KW catalytic subunit of proton-translocating ATPase; antimicrobial;
 KW vaccine; primer; ds.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO200123604-A2.
 XX
 PD 05-APR-2001.
 XX
 XX 28-SEP-2000; 2000WO-CA01150.
 XX
 XX 28-SEP-1999; 99CA-2283458.
 PR 19-MAY-2000; 2000CA-2307010.
 XX
 PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 XX
 PI Bergeron MC, Boissinot M, Huletsky A, Menard C, Ouellette M;
 PI Picard FJ, Roy PH;
 XX
 DR WPI; 2001-24506/25.
 XX
 PT Nucleic acid sequences are used to generate universal probes and
 PT primers which can be used to identify and detect the presence of algal,
 PT archaeal, bacterial, fungal and parasitica species in a test sample -
 XX
 PS Disclosure: Page 1048-1049; 1580pp: English.
 XX
 XX The present invention describes a method for generating a repertoire of
 CC nucleic acids of tuf, fns, atpD and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitica
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
 CC detection and identification of an algal, archaeal, bacterial, fungal
 CC and parasitica species, genus, family and group. A nucleic acid (I)
 CC obtained using the method of the invention can be used for the universal
 CC detection of any bacterium, fungus or parasite in a sample and for the
 CC detection of at least one antimicrobial agent resistance gene or at
 CC least one toxin gene. hexA nucleic acids are used for the specific and
 CC ubiquitous detection and for identification of Streptococcus pneumoniae.
 CC (I) can be used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
 CC which can be detected include Abiotrophia adians, Bordetella sp.,
 CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
 CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
 CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
 CC provides faster results than substrate specificity tests as results can
 CC be determined in an hour and improved accuracy is also achieved.
 CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
 CC which are given in the exemplification of the present invention.
 XX
 XX Sequence 2456 BP; 1001 A; 344 C; 396 G; 715 T; 0 other;
 SO
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 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 AAS93747
 ID AAS93747 standard; CDNA: 301 BP.
 XX
 AC AAS93747;
 XX
 DE 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #29551.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 KW
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US08631.
 PP
 XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 PI
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB: ABG29560.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnosis, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PT
 PS Claim 1; SEQ ID NO 29551; 103pp: English.
 XX
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SO Sequence 301 BP; 64 A; 67 C; 91 G; 79 T; 0 other;
 XX
 Query Match 92.9%; Score 13; DB 23; Length 301;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
AAK72181/c
ID AAK72181 standard; DNA: 422 BP.
XX
AC AAK72181;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26993.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
UF 17-JAN-2001; 2001WO-US01354.
XX
1 31-JAN-2000; 2000US-0179065.
2 04-FEB-2000; 2000US-0180628.
3 24-FEB-2000; 2000US-0184664.
4 02-MAR-2000; 2000US-0186350.
5 16-MAR-2000; 2000US-0189874.
6 17-MAR-2000; 2000US-0190076.
7 18-APR-2000; 2000US-0198123.
8 19-MAY-2000; 2000US-0205515.
9 07-JUN-2000; 2000US-0209467.
10 28-JUN-2000; 2000US-0214886.
11 30-JUN-2000; 2000US-0215135.
12 07-JUL-2000; 2000US-0216647.
13 07-JUL-2000; 2000US-0216880.
14 11-JUL-2000; 2000US-0217487.
15 11-JUL-2000; 2000US-0217486.
16 14-JUL-2000; 2000US-0218290.
17 26-JUL-2000; 2000US-0220963.
18 26-JUL-2000; 2000US-0220964.
19 14-AUG-2000; 2000US-0224518.
20 14-AUG-2000; 2000US-0224519.
21 14-AUG-2000; 2000US-0225213.
22 14-AUG-2000; 2000US-0225214.
23 14-AUG-2000; 2000US-0225266.
24 14-AUG-2000; 2000US-0225267.
25 14-AUG-2000; 2000US-0225268.
26 14-AUG-2000; 2000US-0225270.
27 14-AUG-2000; 2000US-0225447.
28 14-AUG-2000; 2000US-0225757.
29 14-AUG-2000; 2000US-0225758.
30 14-AUG-2000; 2000US-0225759.
31 18-AUG-2000; 2000US-0226279.
32 22-AUG-2000; 2000US-0226681.
33 22-AUG-2000; 2000US-0226868.
34 22-AUG-2000; 2000US-0227182.
35 23-AUG-2000; 2000US-0227009.
36 30-AUG-2000; 2000US-0228924.
37 01-SEP-2000; 2000US-0229287.
38 01-SEP-2000; 2000US-0229344.
39 01-SEP-2000; 2000US-0229345.
40 01-SEP-2000; 2000US-0229345.
41 05-SEP-2000; 2000US-0229509.
42 05-SEP-2000; 2000US-0229513.
43 06-SEP-2000; 2000US-0230437.
44 06-SEP-2000; 2000US-0230438.
45 08-SEP-2000; 2000US-0231242.
46 08-SEP-2000; 2000US-0231243.
47 08-SEP-2000; 2000US-0231244.
48 08-SEP-2000; 2000US-0231413.
49 08-SEP-2000; 2000US-0231414.
50 08-SEP-2000; 2000US-0232080.
51 08-SEP-2000; 2000US-0232081.
52 12-SEP-2000; 2000US-0231968.
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PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 25-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
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PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure: SEQ ID NO 26993; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases or haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention.
XX
XX Sequence 422 BP; 75 A; 124 C; 135 G; 88 T; 0 other:
XX
XX Query Match 92.9%; Score 13; DB 22; Length 422;
XX Best Local Similarity 100.0%; Pred. No. 4.5e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX / 1 GAAGGTGTCTTA 13
XX | | | | | | | | | |
XX DB 419 GAAGGTGTCTTA 407

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Search completed: December 10, 2002, 17:32:30
 Job time : 94.2737 secs

FEATURES Tosoh Corporation (JP)
location/Qualifiers
source 1..20
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/db_xref="taxon:32630"
/note="Oligonucleotide capable of binding specifically to
meca gene or RNA derived from said gene"

BASE COUNT 2 a 3 c 2 g 13 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTTA 20
|||||
1 TTCTTTTATCTTCGGTTA 20

RESULT 2
CUS AX306864 20 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 23 from Patent EP1160333.
ACCESSION AX306864
VERSION AX306864.1 GI:17894686
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Taya,T., Ishiguro,T. and Saito,J.
TITLE Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
JOURNAL Patent: EP 1160333-A 23 05-DEC-2001;
Tosoh Corporation (JP)
location/Qualifiers
source 1..20
/organism="synthetic construct"
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/note="Primer"

BASE COUNT 2 a 3 c 2 g 13 t
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTTA 20
|||||
1 TTCTTTTATCTTCGGTTA 20

RESULT 3
A44526 467 bp DNA linear PAT 07-MAR-1997
LOCUS A44526
DEFINITION Sequence 2 from patent WO9513395.
ACCESSION A44526
VERSION A44526.1 GI:2299344
KEYWORDS
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 467)
AUTHORS Springer,W. and Endermann,R.
TITLE SPECIFIC GENE PROBES AND METHODS FOR QUANTITATIVE DETECTION OF
METHICILLIN-RESISTANT STAPHYLOCOCCI
JOURNAL Patent: WO 9513395-A 2 18-MAY-1995;
BAYER AG (DE)
COMMENT Other publication DE 4338119 950511.
location/Qualifiers
source 1..467
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"

BASE COUNT 187 a 73 c 85 g 122 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 467;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTTA 20
|||||
143 TTCTTTTATCTTCGGTTA 124

RESULT 4
E09772/c 1789 bp RNA linear PAT 29-SEP-1997
DEFINITION The base sequence of modified meca DNA.
ACCESSION E09772
VERSION E09772.1 GI:22026401
KEYWORDS JP 1995209294-A/2.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 1789)
AUTHORS Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
TITLE NOVEL 'MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL Patent: JP 1995209294-A 2 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
COMMENT JP 1995209294-A/2
PN 11-AUG-1995
PD 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
MASAHISA,
PI SUGURO KAZUYA
PC C01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC
C12R1:19),
PC (C12P21/02,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key location/Qualifiers
FH FT source 1..1789
FT FT 1..1608 /organism="Staphylococcus aureus" FT CDS
FT 1..1789 /product="Modified meca".

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source location/Qualifiers
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BASE COUNT 735 a 263 c 302 g 489 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1789;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTTA 20
|||||
768 TTCTTTTATCTTCGGTTA 749

RESULT 5
AR089410/c 2007 bp DNA linear PAT 07-SEP-2000
LOCUS AR089410
DEFINITION Sequence 169 from patent US 5994066.
ACCESSION AR089410
VERSION AR089410.1 GI:10016167
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2007)

AUTHORS Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.
 TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
 JOURNAL Patent: US 5994066-A 169 30-NOV-1999;
 FEATURES Location/Qualifiers
 1..2007
 BASH COUNT 855 a 270 c 341 g 541 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCTTTTATCTTCGGTTA 20
 Db 1167 TTCCTTTTATCTTCGGTTA 1148

RESULT 6
 LOCUS AR093610 2007 bp DNA linear PAT 08-SEP-2000
 DEFINITION Sequence 169 from patent US 6001564.
 ACCESSION AR093610
 VERSION AR093610.1 GI:10020359
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 1 (bases 1 to 2007)
 REFERENCE Bergeron,M.G., Ouellette,M. and Roy,P.H.
 AUTHORS Species specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
 JOURNAL Patent: US 6001564-A 169 14-DEC-1999;
 FEATURES Location/Qualifiers
 1..2007
 BASH COUNT 855 a 270 c 341 g 541 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCTTTTATCTTCGGTTA 20
 Db 1167 TTCCTTTTATCTTCGGTTA 1148

RESULT 7
 SAPP/c 2322 bp DNA linear BCT 12-SEP-1993
 LOCUS Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible penicillin-binding protein.
 ACCESSION Y00868
 VERSION Y00868.1 GI:46628
 KEYWORDS penicillin-binding protein.
 SOURCE Staphylococcus aureus.
 ORGANISM Staphylococcus aureus
 Bacteria; Firmicutes; Bacillales; Staphylococcus.
 1 (bases 1 to 2322)
 REFERENCE Song,M.D., Machi,M., Doi,M., Ishino,F. and Matsubashi,M.
 AUTHORS Evolution of an inducible penicillin-target protein in methicillin-resistant Staphylococcus aureus by gene fusion
 JOURNAL FEBS Lett. 221 (1), 167-171 (1987)
 MEDLINE 87304805
 PUBMED 3305073
 REFERENCE 2 (bases 1 to 2322)
 AUTHORS Ryfel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,

TITLE Barberis-Maino,L., Kayser,F.H. and Berger-Bachl,B.
 Sequence comparison of mecA genes isolated from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis
 JOURNAL Gene 94 (1), 137-138 (1990)
 MEDLINE 91033056
 PUBMED 2227446
 COMMENT Data kindly reviewed (13.1.88) by Matsubashi.
 FEATURES Location/Qualifiers
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 CDS /organism="Staphylococcus aureus"
 /db_xref="taxon:1280"
 1..2013
 /note="penicillin-binding protein (PA 1-670)"
 /codon_start=1
 /transl_table=11
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BASE COUNT 940 a 324 c 389 g 669 t
 ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 2322;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCTTTTATCTTCGGTTA 20
 Db 1173 TTCCTTTTATCTTCGGTTA 1154

RESULT 8
 E03736 2322 bp DNA linear PAT 29-SEP-1997
 LOCUS DNA sequence of PBP2' gene for determination of methicillin resistance.
 DEFINITION
 ACCESSION E03736
 VERSION E03736.1 GI:2171951
 KEYWORDS JP 1992169200-A/9.
 SOURCE unidentified.
 ORGANISM unidentified.
 1 (bases 1 to 2322)
 REFERENCE Matanabe,Y., Nakamura,E., Teraoka,H., Wada,K., Minamide,W. and Murakami,K.
 AUTHORS DETECTION OF PBP 2' GENE AND JUDGEMENT OF METHICILLIN RESISTANCE
 JOURNAL Patent: JP 1992169200-A 9 17-JUN-1992;
 SHIONOGI & CO LTD
 OS (methicillin resistant)staphylococcus aureus
 PN JP 1992169200-A/9
 PD 17-JUN-1992
 PP 31-OCT-1990 JP 1990296708
 PI MATANABE YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI, MINAMIDE WAKIO, MURAKAMI KAZUHIISA
 PC C1201/68,C12N15/11;
 CC strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH Location/Qualifiers

FT misc.feature 1..2322
FT /note="PBP2' gene for determination of
FT methicillin
FT resistance".
FEATURES
source 1..2322
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 939 a 324 c 390 g 669 t
ORIGIN
Query Match 100.0%: Score 20; DB 6; Length 2322;
Best Local Similarity 100.0%: Pred. No. 2,5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCTTTTATCTCGGTTA 20
|||||
Db 1173 TTCTTTTATCTCGGTTA 1154
TSUT 9
MECAPB/C 2454 bp DNA linear BCT 12-SEP-1993
LOCUS 5. epidermidis meca gene for PBP2' (penicillin binding protein 2').
DEFINITION X52592
VERSION X52592.1 GI:46993
KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
penicillin-binding protein 2'.
SOURCE Staphylococcus epidermidis.
ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 2448)
AUTHORS Ryffel,C.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
REFERENCE Medical Microbiology, Gloriast 32, CH-8028 Zuerich, Switzerland
AUTHORS 2 (bases 1 to 2454)
Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,
Barberis-Malno,L., Kayser,F.H. and Berger-Bachli,B.
REFERENCE Sequence comparison of meca genes from methicillin-resistant
AUTHORS Staphylococcus aureus and Staphylococcus epidermidis
TITLE Staphylococcus aureus and Staphylococcus epidermidis
JOURNAL Gene (1990) In press
REFERENCE 3 (bases 1 to 2454)
AUTHORS Ryffel,C.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1990) Ryffel C., University of Zuerich, Inst of
REFERENCE Medical Microbiology, Gloriast 32, CH-8028 Zuerich, Switzerland
AUTHORS 4 (bases 1 to 2454)
Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,
Barberis-Malno,L., Kayser,F.H. and Berger-Bachli,B.
REFERENCE Sequence comparison of meca genes isolated from
AUTHORS methicillin-resistant Staphylococcus aureus and Staphylococcus
epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT See also <X52593-4> and <Y00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.
FEATURES
source Location/Qualifiers
1..2454
/organism="Staphylococcus epidermidis"
/strain="WT5"
/db_xref="taxon:1282"
/clone="WT80/WT79"
80..85
/note="35 region"
101..105
/note="10 region"
130..134
/note="ribosome binding site"
141..2159
/note="primary transcript"
141..2147
CDS

/note="PBP2' (AA 1 - 668)"
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/db_xref="GI:46994"
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/translation="MKKIKYPLILIVVVGFGIYFVASKDEINNTIDATEDKNFKO
VYKDSYISKSDNCEVEKTEPERIKITYSLGKIDINIDRKIKKSKKKKRYDAOKYIK
TNYGNIDRNVOFNFKEDGMKLDMDHSV11PGMOKDOS1H1EN1KSPKCK1LDNRNV
ELANTGTAYEIGIVPKNVSKKDYKAIKAELS1SEDY1IKOQMDXWVDDPVP1PLKTVK
KMEY1LSDFAKFFHLLTNETESRNVPLGKATSHLDGVGP1NSEEL1KOEKYGKYDA
VIGKKLEK1YDKR1LHEDGYRAT1VDNDSMT1AH7L1EKKKKGKDI1OLT1DAKVOK
S1YNNMKNDVSGFA1HPQGGELALVSTPEYDYVPMYGSNEEYK1LEDEKKEPLL
MKRQ1TSPG1STOK1IL1TAM1GLNKT1LDDK1SYK1IDGKQKDK1SMGCGYATREYVN
GN1DLKQ1LES1DN1FF1FARVAL1E1GSKK1FEKGMK1K1GVED11SD1P1FYNAQ1SNKN1
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441..448
/note="altaaac was ac in [1]"
/citation=[1]
old_sequence 641..643
/note="agc was ac in [1]"
old_sequence 652..653
/citation=[1]
old_sequence 731..733
/note="ta was tta in [1]"
old_sequence 780..781
/note="ct was ctt in [1]"
/citation=[1]
BASE COUNT 997 a 345 c 398 g 714 t
ORIGIN
QY 1 TTCTTTTATCTCGGTTA 20
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Db 1307 TTCTTTTATCTCGGTTA 1288
RESULT 10
E09771/c 2455 bp RNA linear PAT 29-SEP-1997
LOCUS The base sequence of meca DNA.
DEFINITION E09771
ACCESSION E09771
VERSION E09771.1 GI:22026400
KEYWORDS JP 1995209294-A/1.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS 1 (bases 1 to 2455)
TITLE Kono,M., Hiratsuyu,K., Sasazu,M., Noguchi,M. and Suguro,K.
JOURNAL NOVEL MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
Patent: JP 1995209294-A 1 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/1
PD 11-AUG-1995
PF 11-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
MASAHISA,
PI SUGURO KAZUYA
PC G01N33/53, C07K14/31, C12N1/21, C12N15/09, C12P21/02, (C12N1/21, PC
C12P1:19)
PC (C12P21/02, C12P1:19):
CC strandedness: Double;
CC topology: Linear;

FEATURES
Source
1.2455
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"

BASE COUNT
997 a 344 c 401 g 713 t

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 2456;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTCGGTTA 20
|||||
b 1306 TTCTTTTATCTCGGTTA 1287

RESULT 11
SAMECAPB 2456 bp DNA linear BCT 12-SEP-1993
LOCUS
DEFINITION S. aureus meca gene for PBP2' (penicillin binding protein 2').
ACCESSION X52593
VERSION X52593.1 GI:46610
KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
penicillin-binding protein 2.
SOURCE Staphylococcus aureus
ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
AUTHORS Ryffel, C.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst. of
Medical Microbiology, Gloriastr. 32, CH-8028 Zuerich, Switzerland
2 (bases 1 to 2456)
REFERENCE
AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P.E.,
Barberis-Maino, L., Kayser, F.H. and Berger-Bachli, B.
TITLE Sequence comparison of meca genes isolated from
methicillin-resistant Staphylococcus aureus and Staphylococcus
epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT See also <X52592>, <X52594> and <Y00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.

FEATURES
Source
1.2456
/organism="Staphylococcus aureus"
/strain="NCTC8325, isolate-BB270"
/db_xref="taxon:1280"
/clone_lib="EMBL-3"
80..85
/note="35 region"
101..105
/note="10 region"
130..134
/note="ribosome binding site"
141..2153
/note="primary transcript"
141..2147
/note="PBP2' (AA 1-668)"
/transl_start=1
/transl_table=1
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/db_xref="GI:46611"
/db_xref="SPTREMBL:Q53707"
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INYNIDRNVOFNFEKEDGMKLDMDHSVILIPGQKDSIHIEMLKSERGKILDRNNY

ELANTGTHRIQIVPKNYSKKDYKAIAKELISIEDYINNNKIKIGYMKIPSEHFRTYK
KMDYLSDFAKKPHILTTNETSRNTPLEKATSHLGIYGPINSELKKEKKGKDDA
VIGKCKLELYDKKLQHEIDGVRVTVDSNSNTIARTLIEKKKOKKIDQITIDAKVOK
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NKPOLTWISPGSTOK1I7FAMIGLNNKTLDDKTSYKIDGGMOKRDKSMGCVNTRVYVN
GNIDLKQAEISSDN1FEFARVALELSKFEKGMKLGVEDIPSDYPPYNAQISNNKL
DNEILLADSGYGOEELINPVOILISYSALENNNGINAPHILKDTKNNVKKNIISKE
NINILNDSQGVNKKTHREKEDIYRSYANIGKSGTALMKKGESGROIGW1ISYDKDN
PMMKATINVKYVOKGMASYNAK1SGKAYDELYENGNKKYVIDE"

BASE COUNT
1001 a 344 c 396 g 715 t

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 2456;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTCGGTTA 20
|||||
Db 1307 TTCTTTTATCTCGGTTA 1288

RESULT 12
AX110445 2456 bp DNA linear PAT 30-APR-2001
LOCUS
DEFINITION Sequence 1178 from Patent WO0123604.
ACCESSION AX110445
VERSION AX110445.1 GI:13926737
KEYWORDS
SOURCE Staphylococcus aureus subsp. aureus NCTC 8325.
ORGANISM Staphylococcus aureus subsp. aureus NCTC 8325.
REFERENCE
AUTHORS Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
Picard, F.J. and Roy, P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1178 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
Source
1.2456
/organism="Staphylococcus aureus subsp. aureus NCTC 8325"
/db_xref="taxon:93061"

BASE COUNT
1001 a 344 c 396 g 715 t

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 2456;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTCGGTTA 20
|||||
Db 1307 TTCTTTTATCTCGGTTA 1288

RESULT 13
SSK8MECA 5596 bp DNA linear BCT 16-JAN-1998
LOCUS
DEFINITION S. sciuri meca gene, strain K8 (ATCC700063).
ACCESSION Y13096
VERSION Y13096.1 GI:2791919
KEYWORDS meca gene; mecI gene; mteRI101; mteRF78; ORF142.
SOURCE Staphylococcus sciuri
ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE
AUTHORS Wu, S., de Lencastre, H. and Tomasz, A.
TITLE Genetic organization of the meca region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus sciuri
JOURNAL J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE 98101461
PUBMED 9440511
REFERENCE
AUTHORS Wu, S.

TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences X53818, X54660, L14020, X52593, 109223.
FEATURES
SOURCE
1. 5596
/organism="Staphylococcus sciuri"
/strain="K8 (ATCC700063)"
/sub_species="rodentius"
/db_xref="taxon:1296"
1. 236
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GRLCTYALYKKNRSLQYCFSPCHEISIMLAS"
complement(485. .856)
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/db_xref="GI:2791921"
/db_xref="SPTREMBL:054285"
/translation="MDNKTYEISSAEDEVNNTIMKKYASANYIEIIONQKMSPT
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VSTPLIPYKISNPFPSKMDMNRNYSDDTSSVHMLDGOSSVTKDLAINNOEPT
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HITISTSSINDPWFGLVKSQIVLPVVEITNDEIEYIILHELSHVSHDLPNO
LYVFKMIFWNPALYISKTMNDCEKVDRLVRLILNHEHIRYGESILKCSILKS
QHINNVAAQYLLGFNSNIKERVYIALYDSMPKRNRIYAYIVCSILLIDAPLS
AHVQODKYEYTNVSYKRLNQLAPYKFGDGSFVLYNERQAYSIYNEPESKORSPNST
YK1YLAIMAFDONLI.SLNHTLOQMDKHOFPKEMODONLNSMKYSVMYVYDNLKAI
LRQDEVKSYDILIEYGNELISGHNENYNESSLKISALPOYVNLKNNKHOMHMFDNKAI
EKVENSNTLKKQDPRKYVCKTGTCGIVNHRKANCFPGYVETKDNITYFATHLKGEDNA
NGEKAOISERITKEMLT"
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complement(2620. .2626)
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complement(2638. .2643)
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2652. .2657
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2676. .2681
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2702. .2707
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2713. .4719
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ELANTGAVEIGIVPKNVSKQDYKAIKELISIEDYINQOMQNNVOJDTVPVPIKTVK
KMDYVLSDFAKKREHLITNETSRNVPLEAKTSHLIGYVPIIASEHILKQKYEYGYDDA
VICKKLEKRLDYKKLOHEDQRYRTIVDQNSNTIAHLLIKKKKIDKDIOJTLIDAKYK
STYNNKNDGSGTAIHPOTGELLALVSTPESVDVYPMGMSNEEYNNKLTEDKKEPL
NKQIITTSPOSTKILITAMIGLNNKTLDDKTSYKIDGKQMDKSGVGNVTRYEVVN
GNIDLQALIESDSNDIFFARVALEIGSKKEKGMKKLGVEIDIPSDYPPYNAQISNNL
DNEIILADSGYGGGELLINPVQIILSTIYSALENNGNINAPHLIKDTKNNYMKNNIISKE
NINLIDGMOQVYVNTKHKEDIYRSVANLIGKSTAEILKKQCHPTGQIQWFIISYDKDN
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complement(4765. .5266)
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complement(4765. .5193)
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/db_xref="SPTREMBL:054520"
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complement(5200. .5205)
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NTEDAKLITRAKAMVKEAGTELWAVTVNPARANOLANNGVDCIIFTDNADKKNVLSQ"
complement(856 c 821 g 1928 t
BASE COUNT 1991 a 856 c 821 g 1928 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 5596;
Best Local Similarity 100.0%; Pred No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCTTTTATCTCGGTA 20
Db 3879 TTCTTTTATCTCGGTA 3860
RESULT 14
SSK3MECA2/c SSK3MECA2 6368 bp DNA linear BCT 16-JAN-1998
LOCUS S.sciuri meca2 gene, strain K3 (MM2).
DEFINITION S.sciuri meca2 gene, strain K3 (MM2).
ACCESSION Y13095
VERSION Y13095.1 GI:2791912
KEYWORDS CTORP261 gene; meca2 gene; mecI gene; mecRI gene; NTORF101; ORP142.
SOURCE Staphylococcus sciuri.
ORGANISM Staphylococcus sciuri

REFERENCE 1 (bases 1 to 6368)
Bacteria: Firmicutes; Bacillales; Staphylococcus.
AUTHORS Wu, S., de lencastre, H. and Tomasz, A.
TITLE Genetic organization of the mecA region in methicillin-susceptible
JOURNAL and methicillin-resistant strains of Staphylococcus sciuri
MEDLINE J. Bacteriol. 180 (2), 236-242 (1998)
PUBMED 9440511
REFERENCE 2 (bases 1 to 6368)
AUTHORS Wu, S.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences U14020, X52593, Y09223.
FEATURES
source location/Qualifiers
1..6368
/organism="Staphylococcus sciuri"
/strain="K3 (MM2)"
/sub_species="rodentius"
/db_xref="taxon:1296"
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complement(<1..784)
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/translation="MENILNINDEKRYLAEIYNHNHISRTQISKNLEINKATISLL
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IKHESYDLPEKVSILSIKIKHIDIEKLDYNGLGVSVSIHGVDNEQHYLPF
HETEGISIAKIKETINVPVVEANMALSALYERNMHNLSYNMLIALSIHKIGIAGL
IINOLYRGANGEGEIGKTLVSKVSDNVEIFHKIEDIFSGEA"
complement(791..797)
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complement(855..860)
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complement(878..883)
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/transl_table=11
/product="MecI protein"
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/db_xref="GI:2791914"
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/translation="MDNKRYEISSAEWEVNNIIMKKYASANNILEIOMQHDSPKT
IKRLITRIYKKCFIDRKKDKIPQYISLVESDITKTKSNFINKVKGGPNSLVLP
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/transl_table=11
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/db_xref="SPTREMBL:O54282"
/translation="MLSSFLMLCIISLLTICVFLVRLMYIKYTONIMKIMLIVL
VSTRLPIPEYKISNTEFSKDMNRRNSPTTSVSHLDQOQSVTDLAINNOEFT
SNITTMILLVFGSLCLFYMIRKARQIDVYIKSSLESSITNERLKVCSKQDYFK
HITISYSSINDNPFGLVKSQIVLPVVEIYNMDEKIEYIIILHLSHVSQDIIFQO
LYVFKMIFENFALYISKTMNDCEKVCDRNKLILNHEHIRYGESILKISILS
OHINNVAAQYILGFNSNIKERVYIALYDSMPKRNKRIVAYIVCSISLLQPLS
AHVQODEFTNVSQILNAPYFKGDSFVLYNEROAYSIYNESPOYSORVSNST
KYIYIAMFARDONLSILNHTQODMKHQPFKEMNODONLSSMKYSVNNYENLNKH
LRQDEKSYDILEYGNELISGDNENTNESISIKSAIEOVNLLKDMQHNHEDNKAI
EKVNSHTLKQDITKYVGKTGTGIVNHEKANGFVGIVETKDTYIFATHLKGEDNA

gene complement(1636..1640)
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complement(3392..3398)
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complement(3410..3415)
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3424..3429
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complement(3433..3438)
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3448..5491
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3448..3453
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3474..3479
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3485..5491
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/transl_table=11
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/db_xref="GI:2791916"
/db_xref="SPTREMBL:O54283"
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VYKSSYISNSDNGEEMTEPRKITYNSLCVQDINODRKIKKVSKKKRGKIDRNV
TNGCNIDRNVFNVKEDGMKILMDHSVLIIPGQKQDSIHILNLSERKILIDRNV
ELANTGAYEIGIYPAKVSCKDYKAIKELISBDYIKOOMDQWVODDFVPLKTYK
KMBEYLSDFAKRHLITNETSRNPLEKATSHLGIVPINSDELKQEKYKGYKQDA
VIGKKGLEKLYDKRLQHEDEGRVITIVDNSNTLAHTLIERKKRDKDIOITIDAKYQ
SIYNNMKNDYSGSTAIHPQTEGLALVSTPSYDVPYPMYQMSDEYKLTEDKEPLL
NKFOITTPSGSTOKILTAMIGLNKTLDDKTSYKIDGQWQKQKSMGGYVWDVAYQ
GNIDKQAISSDSNIFPARVALELGSKPKFKMKGVCVDIPSDYFYNAOISNKL
DNELLADSGVGEELINPQILISYSALENNGNINAPALDLDTKKKKYKKNITSE
NINLTGQMOYVYKTHKEDIYRSANLIGKSGTAEIKMKQGETGRPTGMFISTDKON
PHLMALINVKDVEPKGMASIVAKISGVYDELKNGKKYDIDE"
complement(5537..6038)
/gene="ORF142"
complement(5537..5965)
/gene="ORF142"
/codon_start=1
/transl_table=11
/protein_id="CAA73543.1"
/db_xref="GI:2791917"
/db_xref="SPTREMBL:O54520"
/translation="MKYDDPVGCTFKTKSLHITPEEIIQFATTFDPQYMHIDKNAE
OSRFGIISGMDTLISFRLMVEEGYGEVYAGTOMNNVKFIKPYVPONTLYVIAE
ITNKSITKKEGGLVTSYSTYNEHEIYKGEYVALINNS"
complement(5972..5977)
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complement(6010..6015)
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complement(6062..6368)
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/gene="NTORF101"
/codon_start=2
/transl_table=11
/protein_id="CAA73544.1"
/db_xref="GI:2791918"
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/translation="SFNVVLVLAEEIIMPQYNRVIFHTTSFREDNRLLDYCNATV
NTEBAKLTAKKVKVKEAGVELVTVNKPARANOLANMGVGDIFTDNDKRVHLSQ"

BASE COUNT

2230

a

998

c

884

g

2256

t

/translation="MNFFRYKQFNKDVITVAVGYLRYTLSTYROISETLREGVNVHH
STVYRWQVQEVAPILYQIMKKKKKAYKMRIDETVYIKIGKWSYLYRAIDAGHTLDI
WLRKORDHMSAFAPIKRLIKOPGKPOKXVITPOAPSTKVMAMAKVITAFKLPDCHCTSK
YLNNLIEDDHRIKVKKTRVOSINTAKNTLKGIECTVAKNNRNSIQIYGFSPCHEI
SIMLAS"

BASE COUNT 3099 a 1469 c 1257 g 3222 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 9047;
Best local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCTTTTATCTTCGGTTA 20
|||||
DB 4638 TTCTTTTATCTTCGGTTA 4619

Search completed: December 10, 2002, 20:17:03
Job time : 437.756 secs

PT mRNA -
 XX Claim 1; Page 17; 28pp; English.
 PS
 CC This invention relates to oligonucleotides used for cleaving, detecting
 CC and amplifying the *mecA* gene (associated with methicillin resistance in
 CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
 CC a detection method employing an RNA amplification process, using RNA
 CC derived from the *mecA* gene as template. Also disclosed is a detection
 CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
 CC amplification process in the presence of a complementary oligonucleotide
 CC probe labelled with an intercalated fluorescent dye, where complementary
 CC binding of the probe to the RNA transcription product results in a
 CC change in the fluorescent property relative to that of a situation where
 CC a complex formation is absent, and then measuring the fluorescence
 CC intensity of the reaction solution. The oligonucleotides may be used as
 CC primers or probes, for detecting methicillin-resistant *S. aureus* in
 CC clinical samples. They may also be used therapeutically to inhibit RNA
 CC reverse transcription or translation. These oligonucleotides permit
 CC rapid and very sensitive detection/identification of the *mecA* gene, at a
 CC relatively low temperature without the need for heat denaturation of
 CC target RNA. The present sequence represents a methicillin resistant
 CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
 SQ Sequence 20 BP; 2 A; 3 C; 2 G; 13 T; 0 other;
 XX
 Query Match 100.0%; Score 20; DB 24; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTCTTTTATCTCGGTTA 20
 DB 1 TTCTTTTATCTCGGTTA 20
 ID ABR85923 standard; DNA; 20 BP.
 AC ABR85923;
 XX
 DT 16-AUG-2002 (first entry)
 DE Methicillin resistant *Staphylococcus aureus* detection primer #23.
 XX
 KW Methicillin resistant *Staphylococcus aureus*; MRSA; primer; ss;
 KW *mecA*; probe.
 XX
 SC *Staphylococcus aureus*.
 EP1160333-A2.
 XX
 PD 05-DEC-2001.
 XX
 PF 29-MAY-2001; 2001EP-0112100.
 XX
 PR 29-MAY-2000; 2000JP-0163149.
 PR 09-JUN-2000; 2000JP-0179394.
 XX
 PA (TOXJ) TOSOH CORP.
 XX
 PI Taya T, Ishiguro T, Saito J;
 XX
 DR WPI: 2002-395832/43.
 XX
 PT New oligonucleotide specific for the *mecA* methicillin-resistance gene,
 PT useful for cleavage, detection and amplification of the gene or related
 PT mRNA -
 XX
 PS Claim 5; Page 20; 28pp; English.
 CC This invention relates to oligonucleotides used for cleaving, detecting
 CC and amplifying the *mecA* gene (associated with methicillin resistance in

CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
 CC a detection method employing an RNA amplification process, using RNA
 CC derived from the *mecA* gene as template. Also disclosed is a detection
 CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
 CC amplification process in the presence of a complementary oligonucleotide
 CC probe labelled with an intercalated fluorescent dye, where complementary
 CC binding of the probe to the RNA transcription product results in a
 CC change in the fluorescent property relative to that of a situation where
 CC a complex formation is absent, and then measuring the fluorescence
 CC intensity of the reaction solution. The oligonucleotides may be used as
 CC primers or probes, for detecting methicillin-resistant *S. aureus* in
 CC clinical samples. They may also be used therapeutically to inhibit RNA
 CC reverse transcription or translation. These oligonucleotides permit
 CC rapid and very sensitive detection/identification of the *mecA* gene, at a
 CC relatively low temperature without the need for heat denaturation of
 CC target RNA. The present sequence represents a methicillin resistant
 CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
 SQ Sequence 20 BP; 2 A; 3 C; 2 G; 13 T; 0 other;
 XX
 Query Match 100.0%; Score 20; DB 24; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTCTTTTATCTCGGTTA 20
 DB 1 TTCTTTTATCTCGGTTA 20
 ID AA086977/c
 AA086977 standard; DNA; 467 BP.
 AC AA086977;
 XX
 DT 16-JAN-1996 (first entry)
 DE Polynucleotide probe for methicillin resistant *Staphylococcus aureus*.
 XX
 KW MRSA; methicillin resistant *Staphylococcus aureus*; probe;
 KW hybridisation; *mecA*; MRSE; *Staphylococcus epidermidis*; ss.
 XX
 OS *Staphylococcus aureus*.
 XX
 PN DE4338119-A1.
 XX
 PD 11-MAY-1995.
 XX
 PE 08-NOV-1993; 93DE-4338119.
 XX
 PR 08-NOV-1993; 93DE-4338119.
 XX
 PA (FAHR) BAYER AG.
 XX
 PI Endermann R, Springer W;
 XX
 DR WPI: 1995-180108/24.
 XX
 PT Detection of methicillin resistant *Staphylococcus* - using an
 PT oligo:nucleotide derived from the *mecA* gene
 XX
 PS Claim 2; Page 11; 14pp; German.
 XX
 CC An oligonucleotide probe having the 467 nucleotide sequence shown
 CC isolated from *S. aureus*, is capable of hybridising with the DNA or
 CC RNA of methicillin resistant *S. aureus* (MRSA). The probe is
 CC specifically derived from the *mecA* gene of *S. aureus* and *S. epidermidis*.
 CC The *mecA* gene product has no homology with known PBs
 CC (penicillin-binding proteins). The new probes allow for the rapid
 CC identification of all MRSE, eradicating need for labour intensive in
 CC vitro cultivation and physiological assays.
 XX
 SQ Sequence 467 BP; 187 A; 73 C; 85 G; 122 T; 0 other;

```
Query Match      100.0%; Score 20; DB 16; Length 467;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TTCTTTTATCTCGGTTA 20
        |||||||
        143 TTCTTTTATCTCGGTTA 124

RESULT 4
AAT04536/c
ID      AAT04536 standard; cDNA to mRNA; 1789 BP.
XX
XX      AAT04536;
AC
XX      11-APR-1996 (first entry)
DT
XX
XX      Staphylococcus aureus 'meca' protein coding sequence.
PT
KW      methicillin-resistant Staphylococcus aureus; MKSA; 'meca' protein;
        antibiotic resistance; ds.
OS
XX      Staphylococcus aureus.
XX
XX      Key      Location/Qualifiers
FH      CDS      1..1608
FT      /*tag= a
          /product= 'mec_A' protein
XX
XX      JF07209294-A.
XX
XX      11-AUG-1995.
PD
XX      10-JAN-1994; 94JP-0012226.
PF
XX      10-JAN-1994; 94JP-0012226.
PR
XX      10-JAN-1994; 94JP-0012226.
PA      (DENK-) DENKA SEIKEN KK.
PA      (KAWA/) KAWANO M.
PA      (MITU ) MITSUBISHI CHEM CORP.
XX
XX      WPI: 1995-313917/41.
DR      P-PSDB; AAR80035.
XX
XX      New 'mec A' protein and DNA encoding it - used for the detection of
PT      methicillin-resistant Staphylococcus aureus
PT
        Claim 5; Page 11-13; 15pp; Japanese.
XX
XX      The present sequence codes for the 'mec A' protein which controls
CC      methicillin resistance in methicillin-resistant Staph. aureus. The
CC      'mec A' protein (mol. wt. 40000) is useful for preparation of
CC      antiserum specific for MRSA, thereby allowing methicillin-resistant
CC      and methicillin-sensitive strains to be distinguished. The coding
CC      sequence was obtained by PCR amplification of the mec A sequence
CC      (see AAT04538) using primers AAT04537 and AAT04539.
CC      N.B. in the sequence listing of the patent specification, the
CC      sequence length is stated to be 1785 bp.
XX
XX      Sequence 1789 BP; 735 A; 263 C; 302 G; 489 T; 0 other:
SQ

Query Match      100.0%; Score 20; DB 16; Length 1789;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TTCTTTTATCTCGGTTA 20
        |||||||
        768 TTCTTTTATCTCGGTTA 749

RESULT 5
AAQ28399/c
```

```
ID      AAQ28599 standard; DNA; 2007 BP.
XX
XX      AAQ28599;
AC
XX      19-FEB-1993 (first entry)
DT
XX
XX      Encodes penicillin binding protein PBP2a-27R.
DE
XX      Penicillin; antibiotic; bacteria; methicillin; staphylococci;
KW      soluble; chelating peptide; MRS infection; methicillin resistant;
KW      strain.
XX
XX      Staphylococcus aureus strain 27R.
OS
XX
XX      Key      Location/Qualifiers
FH      CDS      1..2007
FT      /*tag= a
          /product= a
XX
XX      EP505151-A.
XX
XX      23-SEP-1992.
PD
XX      18-MAR-1992; 92EP-0302298.
PF
XX      19-MAR-1991; 91US-0672704.
PR
XX      (ELIL ) LILLY & CO E.L.I.
PA
XX
XX      Blaszcak LC, Skatrud PL, Smith MC, Wu CYE;
PI      WPI: 1992-318034/39.
XX
XX      Polynucleotide cpd. encoding PBP 2a-27R protein or its deriv. -
PT      contains PBP isolated from Staphylococcus aureus and is used to
PT      treat methicillin resistant staphylococci
XX
XX      Disclosure; Page 14; 101pp; English.
XX
XX      This sequence encodes a PBP2a penicillin binding protein isolated
CC      from S. aureus strain 27R. A cDNA library was constructed from
CC      S. aureus DNA in lambda phage EMBL3. Packaging extracts from this were
CC      then used to infect E. coli Cj236. Plaques were screened for the
CC      presence of the mecA-27R gene by a probe produced by PCR amplification
CC      of the mecA gene using primers Q28600.1. Positive plaques were purified
CC      and digested with HindIII, and this fragment digested with XbaI and
CC      cloned into M13mp18 and M13mp19 for sequencing.
XX
XX      Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other:
SQ

Query Match      100.0%; Score 20; DB 13; Length 2007;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TTCTTTTATCTCGGTTA 20
        |||||||
        1167 TTCTTTTATCTCGGTTA 1148

RESULT 6
AAT28568/c
ID      AAT28568 standard; DNA; 2007 BP.
XX
XX      AAT28568;
AC
XX      01-APR-1997 (first entry)
DT
XX
XX      Bacterial antibiotic resistance gene, mecA, probe.
DE
XX
XX      Detection: probe; amplification primer; bacterial pathogen; pneumonia;
KW      Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
KW      Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
KW      Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
KW      Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
KW
```

KM Haemophilus influenzae; Moraxella catarrhalis; septicaemia; meningitis;
 KM infection; intra-abdominal infection; skin infection;
 KM bacterial resistance; beta-lactam antibiotic; ds.
 XX Synthetic.
 OS
 PN MO9608582-A2.
 XX
 XX 21-MAR-1996.
 PD
 XX 12-SEP-1995; 95WO-CA00528.
 PF
 XX 12-SEP-1994; 94US-0304732.
 PR
 XX (BFGC/) BERGHEON M G.
 PA (OUEI/) OUELLETTE M.
 PA (ROY/) ROY P H.
 XX
 PI Bergeron MG, Ouellette M, Roy PH;
 PI
 XX WPI; 1996-179953/18.
 DK
 XX
 PT Method for the detection of bacterial species using probes and
 PT primers - allows detection and quantification of antibiotic
 PS resistant bacteria in patients, the environment and food
 PS
 XX Claim 91: Page 144-145; 216pp: English.
 CC The sequences given in AAT8560-76 represent fragments derived from
 CC bacterial antibiotic resistance genes which were used as probes in the
 CC method of the invention for the detection of bacterial species in a
 CC sample. The method of the invention comprises using probes and/or
 CC amplification primers which are specific, ubiquitous and sensitive for
 CC determining the presence and/or amount of nucleic acids from selected
 CC bacterial species in any sample, where the bacterial nucleic acid
 CC comprises a selected target region hybridisable with the probes or
 CC primers. The method comprises contacting the sample with the probes or
 CC primers or amplification products as and indication of the presence
 CC and/or amount of the bacterial species. This method may be used to
 CC detect commonly encountered bacterial pathogens, e.g. Escherichia coli,
 CC Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis,
 CC Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus
 CC epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus,
 CC Streptococcus pyogenes, Haemophilus influenzae and Moraxella
 CC catarrhalis. These bacterial species are associated with approx. 90% of
 CC urinary tract infections and with a high percentage of other severe
 CC infections including septicaemia, meningitis, pneumonia, intra-abdominal
 CC infections, skin infections and other severe respiratory tract
 CC infections. The method may also be used to evaluate a bacterial
 CC resistance to beta-lactam antibiotics.
 XX
 3 Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
 Query Match 100.0%; Score 20; DB 17; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTCTTTTATCTTCGCTTA 20
 DB 1167 TTCTTTTATCTTCGCTTA 1148
 AAV68337/C
 ID AAV68337 standard; DNA; 2007 BP.
 AC AAV68337;
 XX
 XX 21-JUN-1999 (first entry)
 DT
 XX Penicillin binding protein PBP2A meca-27R gene of S. aureus 27R.
 DE
 XX

KM Penicillin binding protein: PBP2A-27R; meca-27R gene;
 KM methicillin resistance; antibiotic; assay; purification; ss.
 XX Staphylococcus aureus.
 OS
 PN EP875578-A2.
 XX
 XX 04-NOV-1998.
 PD
 XX 18-MAR-1992; 92EP-0302298.
 PF
 XX 19-MAR-1991; 91US-0672704.
 PR
 XX (ELIL) LILLY & CO ELI.
 PA
 XX Blaszcak LC, Skatrud PL, Smith MC, Wu CE;
 PI
 XX WPI; 1998-559443/48.
 DR P-PSDB; AAW81149.
 XX
 PT New Staphylococcus aureus soluble penicillin-binding proteins and
 PT their derivatives - useful for screening for compounds effective
 PS against methicillin resistant organisms
 PS
 XX Disclosure; Page 14-16; 97pp: English.
 CC This meca-27R gene encodes penicillin binding protein 2A (PBP2A-27R)
 CC responsible for the methicillin resistance of Staphylococcus aureus
 CC strain 27R. The invention provides new PBPs of formula SP-I..-PBP2As,
 CC where: SP is 0 or a signal peptide (preferably from the ampc, ompA or
 CC beta-lactamase gene product); L is Met-Val or a compound of formula
 CC AAW81151-58) of formula (His)x-(Ala)y-(His)z and A-an amino acid, (see
 CC x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above,
 CC polypeptide where each monomer unit is the same or different; Pro
 CC is proline, n = 0 or 1; and PBP2As is soluble PBP2A-27R protein (see
 CC AAW81159-62). Also claimed are polynucleotides encoding specific
 CC soluble PBP2A compounds. The new PBP2A-27R proteins are useful for
 CC assaying for agents useful as antibiotics against methicillin
 CC resistant Staphylococcus strains by creating a kinetically inert
 CC complex between a support-immobilised transition ion and a modified
 CC soluble PBP2A protein comprising a chelating agent, which screens
 CC for agents which bind to PBP2A proteins (disclosed). Soluble forms
 CC of PBP2A-27R protein facilitate crystallisation as they lack their
 CC transmembrane association region, and so are useful for x-ray
 CC crystallography studies of the protein, assisting in the design of
 CC antibiotic compounds against methicillin resistant Staphylococcus
 CC strains (disclosed). The chelating peptide operably linked to the
 CC BPA-27R proteins is useful for purifying PBPs.
 XX
 50 Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
 Query Match 100.0%; Score 20; DB 19; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTCTTTTATCTTCGCTTA 20
 DB 1167 TTCTTTTATCTTCGCTTA 1148
 ABA76993/C
 ID ABA76993 standard; DNA; 2007 BP.
 AC ABA76993;
 XX
 XX 28-JAN-2002 (first entry)
 DT
 XX Antibiotic resistance detection polynucleotide SEQ ID NO 169.
 DE
 XX Detection: bacterial species: animal; food; environment;
 KM antibiotic resistance; ds.

XX	Unidentified.
OS	
XX	
XX	
PN	NZ501596-A.
XX	
PD	29-JUN-2001.
XX	
XX	
XX	12-SEP-1995; 95NZ-0501596.
PR	12-SEP-1995; 95NZ-0501596.
XX	
XX	
PA	(ID11-) ID1 INFECTIO DIAGNOSTIC INC.
P1	Bergeron MG, Ouellette M, Roy PH;
DR	WPI: 2001-615034/71.
XX	
XX	
PT	Method for detecting target bacterial species in a sample, comprises
PT	detecting the presence or amount of bacterial nucleic acid amplified by
PT	a primer derived from bacterial DNA, specific for the target bacterial
PT	species -
XX	
PS	Claim 16; Page 159-160; 168pp; English.
XX	
CC	The invention relates to detecting target bacterial species suspected to
CC	be present in a sample, comprising contacting nucleic acids of target
CC	bacterial species with an amplification primer pair derived from a
CC	bacterial DNA fragment (ABA76825-ABA76861) specific for the target
CC	bacterial species but ubiquitous for different strains, amplifying the
CC	nucleic acid and detecting the presence or amount of an amplified
CC	sequence as an indication of the presence or amount of the target
CC	bacterial species. The invention includes primers and probes
CC	(ABA76862-ABA76984) against the target bacterial species, especially
CC	E.coli, K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae,
CC	S.aureus, S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes,
CC	H.influenzae, M.catarhalis and/or group A Streptococci producing
CC	exotoxin A gene spe A, suspected to be present in a sample which is
CC	obtained from human patients, animals, environment or food, and which
CC	consists of one or more bacterial colonies. Oligonucleotide
CC	probes and primers complementary to the bacterial genes encoding
CC	resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aadB,
CC	aacC1, aacC2, aacC3, aacA4, mecA, vanA, vanH, vanX, satA, aacA-aphD, vat,
CC	vga, msrA, sul and/or int (ABA76985-ABA77001) are also useful to identify
CC	commonly encountered and clinically important resistance genes. The
CC	invention provides a rapid method of bacterial identification that can be
CC	achieved, which reduces the time currently required for the
CC	identification of pathogens in the clinical laboratory.
XX	
SQ	Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
XX	
Query Match	100.0%; Score 20; DB 22; Length 2007;
Best Local Similarity	100.0%; Pred. NO. 35;
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
XX	
YY	1 TTTCTTTTATTCCTGCGTTA 20
DB	1167 TTTCTTTTATTCCTGCGTTA 1148
XX	
RESULT 9	
ABN92247/c	
ID	ABN92247 standard; DNA; 2028 BP.
XX	
XX	ABN92247;
XX	
DT	24-JUL-2002 (first entry)
DE	Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1710.
XX	
KM	Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KM	antibacterial; gene therapy; gene; ds.
XX	
OS	Staphylococcus epidermidis.

XX	US6380370-B1.	
PN		
XX		
PD	30-APR-2002.	
XX		
XX		
PF	13-AUG-1998;	98US-0134001.
XX		
PR	14-AUG-1997;	97US-055779P.
PR	08-NOV-1997;	97US-064964P.
XX		
PA	(GENO-) GENOME THERAPEUTICS CORP.	
XX		
PI	Doucette-Stamm LA, Bush D;	
XX		
DR	WPI: 2002-381255/41.	
DR	P-PSDB; ABP39702.	
XX		
PT	Novel isolated nucleic acid encoding a Staphylococcus epidermidis	
PT	polypeptide, useful for diagnosing and treating bacterial infections -	
PS		
XX	Disclosure; SEQ ID 1710; 267pp; English.	
CC		
CC	ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading	
CC	frame (ORF) nucleic acid sequences which encode the amino acid sequences	
CC	given in ABP35124 to ABP37960. The S. epidermidis sequences have	
CC	antibacterial activity and can be used in gene therapy. The sequences	
CC	can also be used in the diagnosis and treatment of bacterial infections,	
CC	particularly S. epidermidis infections. The sequences can be used to	
CC	screen for compounds able to interfere with the S. epidermidis life	
CC	cycle or inhibit S. epidermidis infection.	
CC	N.B. The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from the	
XX	USPTO web site.	
XX		
SQ	Sequence 2028 BP; 861 A; 273 C; 346 G; 547 T; 1 other:	
	Query Match	100.0%; Score 20; DB 24; Length 2028;
	Best local Similarity	100.0%; Pred. No. 35;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TTCCTTTTATCTTCGGTTA 20	
DB	1188 TTCCTTTTATCTTCGGTTA 1169	
	RESULT 10	
	AAQ35213/c	
ID	AAQ35213 standard; DNA; 2110 BP.	
XX		
AC	AAQ35213;	
XX		
DT	06-JUN-1993 (first entry)	
XX		
DE	Sequence of the mcc A gene.	
XX		
KW	Mechicillin-resistant staphylococci; detection; primer; PCR; ss.	
OS		
XX	Staphylococcus aureus.	
FT	Key	Location/Qualifiers
FT	CDS	105..2110
FT		/*tag= a
XX		
PN	EP527628-A.	
XX		
PD	17-FEB-1993.	
XX		
PF	10-AUG-1992;	92EP-0307307.
XX		
PR	13-AUG-1991;	91US-0744770.
XX		
PA	(ELIL) LILLY & CO ELI.	
XX		

PI Skatrud PL, Unal S;
 XX
 DR WPI: 1993-054352/07.
 DR P-PSDB; AAR30845.
 XX
 PT
 PT Detection of methicillin-resistant staphylococci - using
 PT sensitive and accurate detection
 XX
 PS Disclosure; Pages 7-10; 16pp; English.
 XX
 CC The inventors claim a method for detecting methicillin-resistant
 CC staphylococcal infections which involves the use of the PCR primed
 CC by fragments of the staphylococcus meca gene. More specifically, the
 CC initial primers used are nucleotides 141-160 and the inverse
 CC complement of nucleotides 1929-1952 of the S. aureus meca gene.
 CC The interior primers are nucleotides 568-593 and the inverse complement
 CC of 1647-1670 of the S. aureus meca gene.
 XX
 SO Sequence 2110 BP; 896 A; 290 C; 350 G; 574 T; 0 other;
 Query Match 100.0%; Score 20; DB 14; Length 2110;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 TTCTTTTATCTTCGGTTA 20
 Db 1271 TTCTTTTATCTTCGGTTA 1252

RESULT 11
 AA025905/c
 ID AA025905 standard; DNA; 2322 BP.
 XX
 AC AA025905;
 XX
 DT 18-JAN-1993 (first entry)
 XX
 DE PBP2'.
 XX
 KM Polymerase chain reaction; PCR; amplification; ss.
 OS
 XX Synthetic.
 FH Key location/Qualifiers
 FT misc_binding 1581..1598
 FT /tag= a
 FT /label= Probe_binding_site
 XX
 PN JP04169200-A.
 PD
 XX 17-JUN-1992.
 XX
 PF 31-OCT-1990; 90JP-0296708.
 31-OCT-1990; 90JP-0296708.
 (SHIO) SHIONOGI & CO LTD.
 WPI: 1992-253403/31.
 DR
 XX
 PT Detection of PBP2' gene for determ. of methicillin-resistance -
 PT useful esp. for detection of methicillin-resistance -
 PT Staphylococcus aureus
 XX
 PS Disclosure; Fig 1; 9pp; Japanese.
 CC The sequence given is the PBP2' gene. This gene could be detected
 CC by the primer sequences given in AA025897-904. Due to the results of
 CC this amplification reaction resistance to methicillin in Staphylococcus
 CC aureus could be determined.
 XX
 SO Sequence 2322 BP; 940 A; 324 C; 389 G; 669 T; 0 other;

Query Match 100.0%; Score 20; DB 13; Length 2322;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 TTCTTTTATCTTCGGTTA 20
 Db 1173 TTCTTTTATCTTCGGTTA 1154

RESULT 12
 AAT04538/c
 ID AAT04538 standard; CDNA to mRNA; 2455 BP.
 XX
 AC AAT04538;
 XX
 DT 11-APR-1996 (first entry)
 XX
 DE Staphylococcus aureus meca protein coding sequence.
 XX
 KM methicillin-resistant Staphylococcus aureus; MRSA; 'meca protein';
 KW antibiotic resistance; ds.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key location/Qualifiers
 FT CDS 134..2146
 FT /tag= a
 FT /product= mec_A-protein
 XX
 PN JP07209294-A.
 PD
 XX 11-AUG-1995.
 XX
 PE 10-JAN-1994; 94JP-0012226.
 XX
 PR 10-JAN-1994; 94JP-0012226.
 XX
 PA (DENK-) DENKA SEIKEN KK.
 PA (KAWA/) KAWANO M.
 PA (MITU) MITSUBISHI CHEM CORP.
 XX
 DR WPI: 1995-313917/41.
 DR P-PSDB; AAR80036.
 XX
 PT New 'mec A' protein and DNA encoding it - used for the detection of
 PT methicillin-resistant Staphylococcus aureus
 XX
 PS Example 2; Page 8-10; 15pp; Japanese.
 CC The present sequence codes for the mec A protein. DNA coding for
 CC the 'mec A' protein, which controls methicillin resistance in
 CC methicillin-resistant Staph. aureus (MRSA), was obtained by PCR
 CC amplification of the mec A sequence using primers AAT04537 and
 CC AAT04539. The 'mec A' protein (mol. wt. 40000) is useful for
 CC preparation of antiserum specific for MRSA, thereby allowing
 CC methicillin-resistant and methicillin-sensitive strains to be
 CC distinguished.
 XX
 SO Sequence 2455 BP; 997 A; 344 C; 401 G; 713 T; 0 other;
 Query Match 100.0%; Score 20; DB 16; Length 2455;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 TTCTTTTATCTTCGGTTA 20
 Db 1306 TTCTTTTATCTTCGGTTA 1287

RESULT 13
 AAH01187/c
 ID AAH01187 standard; DNA; 2456 BP.

```

XX AC AAH01187;
XX DT
XX DE 24-JUL-2001 (first entry)
XX DE Staphylococcus aureus nucleotide sequence SEQ ID NO:1178.
XX DE
XX DE Species specific; genus specific; family specific; probe; detection;
XX DE Identification; algal; archaeal; bacterial; fungal; parasitic;
XX DE microorganism; diagnosis; translation elongation factor Tu; toxin;
XX DE translation elongation factor G; RecA recombinase; resistance;
XX DE catalytic subunit of proton-translocating ATPase; antimicrobial;
XX DE vaccine; primer; ds.
XX OS Staphylococcus aureus.
XX PN
XX PN WO200123604-A2.
XX PN
XX PN 05-APR-2001.
XX PN
XX PN 28-SEP-2000; 2000WO-CN01150.
XX PR 28-SEP-1999; 99CA-2283458.
XX PR 19-MAY-2000; 2000CA-2307010.
XX PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
XX PI Picard FJ, Roy PH.
XX DR WPI: 2001-245006/25.
XX PT Nucleic acid sequences are used to generate universal probes and
XX PT primers which can be used to identify and detect the presence of algal,
XX PT archaeal, bacterial, fungal and parasitical species in a test sample.
XX PS Disclosure: Page 1048-1049; 1580pp; English.
XX PS
XX CC The present invention describes a method for generating a repository of
XX CC nucleic acids of tuf, fus, atpd and/or recA genes from which probes
XX CC and/or primers are derived. The method comprises amplifying the nucleic
XX CC acids of determined algal, archaeal, bacterial, fungal and parasitical
XX CC species with a combination of defined primer pairs. The method can be
XX CC used for producing probes and/or primers for detecting one or more
XX CC related microorganisms e.g. algae, archaea, bacteria, fungi and
XX CC parasites, for universal detection and for specific, bacterial, fungal
XX CC detection and identification of an algal, archaeal, bacterial, fungal
XX CC and parasitical species, genus, family and group. A nucleic acid (I)
XX CC obtained using the method of the invention can be used for the universal
XX CC detection of any bacterium, fungus or parasite in a sample and for the
XX CC detection of at least one antimicrobial agent resistance gene or at
XX CC least one toxin gene. hexA nucleic acids are used for the specific and
XX CC ubiquitous detection and for identification of Streptococcus pneumoniae.
XX CC (I) can be used to design a therapeutic agent which is effective against
XX CC microorganisms. Microbial species or genus or family or phylum or group
XX CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
XX CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
XX CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
XX CC Neisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests
XX CC provides faster results than substrate specificity tests as results can
XX CC be determined in an hour and improved accuracy is also achieved.
XX CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
XX CC which are given in the exemplification of the present invention.
XX SQ
SQ Sequence 2456 BP; 1001 A; 344 C; 396 G; 715 T; 0 other:
Query Match 100.0%; Score 20; DB 22; Length 2456;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCTTTTATCTTCGCTTA 20
DB 1307 TTCTTTTATCTTCGCTTA 1288

```

```

RESULT 14
AAAX20260/C
ID AAAX20260 standard; DNA: 9542 BP.
XX
XX AC AAAX20260;
XX DT
XX DE 04-MAY-1999 (first entry)
XX DE
XX DE Borrelia burgdorferi polynucleotide sequence #13.
XX DE
XX DE Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;
XX DE epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
XX DE infection; diagnosis; characterisation; detection; ds.
XX OS
XX OS Borrelia burgdorferi.
XX PN
XX PN WO9858943-A1.
XX PN
XX PN 30-DEC-1998.
XX PN
XX PF 18-JUN-1998; 98WO-US12764.
XX PR
XX PR 03-SEP-1997; 97US-0057483.
XX PR 20-JUN-1997; 97US-0050359.
XX PR 22-JUL-1997; 97US-0053344.
XX PR 22-JUL-1997; 97US-0053377.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (MED1-) MEDIMUNE INC.
XX PI Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO;
XX PI White OR.
XX DR WPI: 1999-081217/07.
XX DR
XX PT New isolated Borrelia burgdorferi nucleic acids - used to develop
XX PT products for the detection, diagnosis, characterisation, prevention
XX PT and therapy of infections, particularly Lyme disease
XX PS Claim 1; Page 920-925; 1128pp; English.
XX PS
XX CC AAAX20248 to AAAX20402 represent polynucleotide sequences isolated from
XX CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for
XX CC the detection, diagnosis, characterisation, prevention and therapy of
XX CC Bb infections, e.g. Lyme disease. They can also be used for the
XX CC production of biosynthetic products, e.g. enzymes. Borrelia belongs
XX CC to a family of motile, spiral-shaped bacteria called Spirochetes.
XX CC Spirochetes are pathogenic in humans and Borrelia causes epidemic and
XX CC endemic relapsing fever, and Lyme borreliosis, more commonly known as
XX CC Lyme disease.
XX SQ
SQ Sequence 9542 BP; 3812 A; 1160 C; 1113 G; 3457 T; 0 other:
Query Match 92.0%; Score 18.4; DB 20; Length 9542;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTCTTTTATCTTCGCTTA 20
DB 4253 TTCTTTTATCTTCGCTTA 4234

```

```

RESULT 15
ABK73798/C
ID ABK73798 standard; DNA: 910 BP.
XX
XX AC ABK73798;
XX DT
XX DE 13-AUG-2002 (first entry)
XX DE
XX DE Bacillus licheniformis genomic sequence tag (GSTR) #1089.
XX DE

```

Sequence 910 BP; 248 A; 217 C; 262 G; 183 T; 0 other;

Search completed: December 10, 2002, 17:32:38
Job time : 133.391 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 : Search time 36.2905 Seconds
(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-22

Perfect score: 28
Sequence: 1 aagaagaaagatgcgaagatattcaa 28

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCY_NEM_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEM_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	10	US-09-865-579A-22
2	28	100.0	39	10	US-09-865-579A-28
3	28	100.0	2007	10	US-09-452-599-169
4	20.6	73.6	2429	10	US-09-764-864-69
5	20.6	73.6	368004	10	US-09-949-854-3
6	20.2	72.1	180557	12	US-10-003-806-6
7	20.2	72.1	180557	12	US-10-003-806-9
8	20	71.4	429	10	US-09-960-352-2449
9	20	71.4	1665	9	US-09-938-842A-3442
10	19.6	70.0	143	10	US-09-974-300-3560
11	19.6	70.0	173	10	US-09-923-876-946
12	19.6	70.0	189	10	US-09-878-574-7719
13	19.6	70.0	254	10	US-09-878-574-5615
14	19.6	70.0	260	10	US-09-878-574-8576
15	19.6	70.0	264	10	US-09-878-574-10488
16	19.6	70.0	266	10	US-09-878-574-10469
17	19.6	70.0	360	10	US-09-878-574-2202
18	19.6	70.0	389	10	US-09-878-574-2715
19	19.6	70.0	393	10	US-09-878-574-3731

20	19.6	70.0	413	10	US-09-878-574-3703	Sequence 3703, Ap
21	19.6	70.0	2153	10	US-09-917-800A-1599	Sequence 1599, Ap
22	19.6	70.0	57130	10	US-09-835-081-3	Sequence 3, App11
23	19.2	68.6	16484	10	US-09-070-927A-158	Sequence 158, App
24	19.2	67.9	281	10	US-09-867-701-8891	Sequence 8891, Ap
25	19	67.9	311	9	US-10-046-935-1802	Sequence 1802, Ap
26	19	67.9	311	9	US-09-878-178-1802	Sequence 1802, Ap
27	19	67.9	340	10	US-09-777-564-272	Sequence 272, App
28	19	67.9	346	10	US-09-878-574-2152	Sequence 2152, Ap
29	19	67.9	380	10	US-09-964-824A-349	Sequence 349, App
30	19	67.9	380	10	US-09-880-107-1135	Sequence 1135, Ap
31	19	67.9	389	10	US-09-960-352-7839	Sequence 7839, Ap
32	19	67.9	391	10	US-09-867-701-9233	Sequence 9233, Ap
33	19	67.9	569	10	US-09-777-564-463	Sequence 463, App
34	19	67.9	2290	10	US-09-764-864-332	Sequence 332, App
35	19	67.9	3694	10	US-09-764-864-329	Sequence 329, App
36	19	67.9	397658	10	US-09-813-320-3	Sequence 3, App11
37	18.8	67.1	330	10	US-09-878-574-615	Sequence 615, App
38	18.8	67.1	29607	10	US-09-764-877-3626	Sequence 3626, Ap
39	18.6	66.4	446	10	US-09-974-300-5765	Sequence 5765, Ap
40	18.6	66.4	897	10	US-09-070-927A-845	Sequence 845, App
41	18.6	66.4	2000	9	US-09-938-842A-4638	Sequence 4638, Ap
42	18.6	66.4	2000	9	US-09-938-842A-4638	Sequence 4638, Ap
43	18.6	66.4	6156	10	US-09-842-256-1	Sequence 1, App11
44	18.6	66.4	21129	10	US-09-764-869-1734	Sequence 1734, Ap
45	18.4	65.7	242	10	US-09-867-701-286	Sequence 286, App

ALIGNMENTS

RESULT 1
US-09-865-579A-22
Sequence 22, Application US/09865579A
Patent NO. US20020098492A1
GENERAL INFORMATION:
APPLICANT: Taya, Toshiki
APPLICANT: Ishiguro, Takahiko
TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
TITLE REFERENCE: 9558-003-27
CURRENT FILING DATE: 2001-05-29
CURRENT APPLICATION NUMBER: JP 2000-163149
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-179394
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-865-579A-22
Query Match 100.0% Score 28; DB 10; Length 28;
Best local Similarity 100.0% Pred. No. 0.077;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AAAGAAAAGTGCAGCAAGATATTCAA 28
Db 1 AAAGAAAAGATGCAGCAAGATATTCAA 28
RESULT 2
US-09-865-579A-28/C
Sequence 28, Application US/09865579A
Patent NO. US20020098492A1
GENERAL INFORMATION:
APPLICANT: Taya, Toshiki


```

; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 28
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-865-579A-28
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Query Match          100.0%; Score 28; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AAAGAAAAAAGATGCCAAAGATATTCAA 28
Db 33 AAAGAAAAAAGATGCCAAAGATATTCAA 6
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RESULT 3
US-09-452-599-169
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Hergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169
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Query Match          100.0%; Score 28; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AAAGAAAAAAGATGCCAAAGATATTCAA 28
Db 948 AAAGAAAAAAGATGCCAAAGATATTCAA 975
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RESULT 4
US-09-764-864-69
; Sequence 69, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
```

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; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior Application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 69
; LENGTH: 2429
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2299)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2359)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2362)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2386)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-69
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```

Query Match          73.6%; Score 20.6; DB 10; Length 2429;
Best Local Similarity 85.2%; Pred. No. 65;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 1 AAAGAAAAAAGATGCCAAAGATATTCA 27
Db 1570 AAAGAAAAAAGATGCCAAAGATATTCA 1596
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```

RESULT 5
US-09-949-654-3
; Sequence 3, Application US/09949654
; Patent No. US20020127644A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000817
; CURRENT APPLICATION NUMBER: US/09/949,654
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/231,572
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 368004
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(368004)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-654-3
```

```

Query Match          73.6%; Score 20.6; DB 10; Length 368004;
Best Local Similarity 85.2%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```

QY 1 AAAGAAAAAAGATGCCAAAGATATTCA 27
Db 39518 AAAGAAAAAAGATGCCAAAGATATTCA 39544
```

```

RESULT 6
US-10-003-806-6
; Sequence 6, Application US/10003806
; Patent No. US20020119929A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Bishop, Colin E.
; APPLICANT: Agoulalik, Alexander I.
; APPLICANT: Zhu, Qichao
; TITLE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY
; FILE REFERENCE: P0206051/10024824
; CURRENT APPLICATION NUMBER: US/10/003,806
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,872
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 180557
; TYPE: DNA
; ORGANISM: Human
US-10-003-806-6
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Query Match      72.1%; Score 20.2; DB 12; Length 180557;
Best Local Similarity 88.0%; Pred. NO. 1.7e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 AAAGAAAAAGATGCCAAGATATT 25
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Db 46438 AAAGTAAAAAGATGACAAAATATT 46462
```

```
RESULT 7
US-10-003-806-9
; Sequence 9, Application US/10003806
; Patent No. US2002011929A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Colin E.
; APPLICANT: Agoulalik, Alexander I.
; APPLICANT: Zhu, Qichao
; TITLE OF INVENTION: CAN 1 AND ITS ROLE IN MAMMALIAN INFERTILITY
; FILE REFERENCE: P0206051/10024824
; CURRENT APPLICATION NUMBER: US/10/003,806
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,872
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 180557
; TYPE: DNA
; ORGANISM: Human
US-10-003-806-9
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Query Match      72.1%; Score 20.2; DB 12; Length 180557;
Best Local Similarity 88.0%; Pred. NO. 1.7e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 AAAGAAAAAGATGCCAAGATATT 25
      ||| ||||| ||| ||| |||
Db 46438 AAAGTAAAAAGATGACAAAATATT 46462
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```
RESULT 8
US-09-960-352-2449/C
; Sequence 2449, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengding
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
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; SEQ ID NO 2449
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 11-L1B3058-031-Q1-K1-C11
US-09-960-352-2449
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Query Match      71.4%; Score 20; DB 10; Length 429;
Best Local Similarity 82.1%; Pred. NO. 81;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY      1 AAAGAAAAAGATGCCAAGATATCAA 28
      ||||| | ||||| ||| |||
Db 145 AAAGAAAGTATGCGCAAGTCTTCAA 118
```

```
RESULT 9
US-09-938-842A-3442
; Sequence 3442, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: S02P1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3442
; LENGTH: 1665
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3442
```

```
Query Match      71.4%; Score 20; DB 9; Length 1665;
Best Local Similarity 82.1%; Pred. NO. 1e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      1 AAAGAAAAAGATGCCAAGATATCAA 28
      ||||| ||| ||| ||| ||| |||
Db 1001 AAAGAAAAATATGGAATAGATTAAA 1028
```

```
RESULT 10
US-09-974-300-3560
; Sequence 3560, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 3560
; LENGTH: 143
; TYPE: DNA
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Query Match	70.08; Score 19.6;
Best Local Similarity	84.68; Pred. No. 99;

RESULT 15

RESULT 15
US-09-878-574-10488

```
; Sequence 10488, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ. ID NOS: 15775
; SEQ. ID NO 10488
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700966730H1
; US-09-878-574-10488

Query Match      70.0%; Score 19.6; DB 10; Length 264;
Best Local Similarity 84.6%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```
QY      1  AAAGCAAAAAGATCGCAAGATATTC 26
      ||| | ||||| ||| ||| |||
Db      84  AAAGTATTAAGATGCGAGACATTC 109
```

Search completed: December 11, 2002, 06:09:17
Job time : 149.29 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 ; Search time 1435.66 Seconds
(without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579A-22

Perfect score: 28

Sequence: 1 aaagaaaaagatgcagaagatattcaa 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_estrc:*
9: qb_estl1:*
10: qb_estl2:*
11: qb_hlc:*
12: qb_estl3:*
13: qb_estl4:*
14: qb_estl5:*
15: em_estfun:*
16: em_estlom:*
17: qb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.2	82.9	613	17	BH009254 ef26a02.x
2	23.2	82.9	707	17	BH532191 BCGP68TF
3	23.2	82.9	921	17	CNS06Y01 AL421343 T7 end of
4	22.8	81.4	618	10	AM255568 M604 pep
5	22.2	79.3	360	17	AQ283551 RPT111-77
6	21.6	77.1	353	14	BH875833 1f86d03.x

7	21.6	77.1	375	10	BH841882	BH841882
8	21.6	77.1	443	14	W89911	W89911 mf76c12.r1
9	21.6	77.1	470	13	B1466683	B1466683 1e25908.y
10	21.6	77.1	507	9	A1430420	A1430420 m176c12.y
11	21.6	77.1	589	17	A2216057	A2216057 Sheared D
12	21.6	77.1	621	17	AQ487311	AQ487311 RPT-11-2
13	21.6	77.1	636	10	BH642313	BH642313 BH642313
14	21.6	77.1	639	10	BH660787	BH660787 BH660787
15	21.6	77.1	685	17	BH029119	BH029119 RPT-24-3
16	21.6	77.1	690	9	A1526147	A1526147 pc3-2.D06
17	21.6	77.1	716	17	BH029113	BH029113 RPT-24-3
18	21.6	77.1	749	13	B1660259	B1660259 603302656
19	21.6	77.1	793	17	AG108121	AG108121 Pan tregl
20	21.6	77.1	876	14	B0895101	B0895101 AGFNCOURT
21	21.2	75.7	235	12	BE171087	BE171087 RPT2036.M
22	21.2	75.7	550	9	A1820785	A1820785 y161c02.y
23	21.2	75.7	572	9	A1668612	A1668612 y161c02.y
24	21.2	75.7	581	17	AQ425329	AQ425329 CITBI-E1-
25	21.2	75.7	726	17	AG125961	AG125961 Pan tregl
26	21.2	75.7	882	17	BH138799	BH138799 EMTNE31TF
27	21.2	75.7	1040	17	BH162219	BH162219 EMTOR25TF
28	20.8	74.3	433	17	A2150645	A2150645 SP_0039_B
29	20.8	74.3	509	17	AQ558792	AQ558792 HS_2067_B
30	20.8	74.3	927	17	BH135840	BH135840 EMTOR83TR
31	20.6	73.6	343	9	A1018760	A1018760 ov28h05.x
32	20.6	73.6	369	10	AW970299	AW970299 EST382380
33	20.6	73.6	374	12	AL757658	AL757658 Arabidops
34	20.6	73.6	388	9	BG602883	BG602883 EST501973
35	20.6	73.6	415	10	BE552194	BE552194 am61a02.x
36	20.6	73.6	418	10	AW232707	AW232707 t124911.x
37	20.6	73.6	447	10	BH730538	BH730538 BS_30538
38	20.6	73.6	480	17	AQ203600	AQ203600 HS_3103_B
39	20.6	73.6	485	9	AA797561	AA797561 vw25b03.r
40	20.6	73.6	494	9	A1650954	A1650954 wa96a11.x
41	20.6	73.6	495	12	BG741432	BG741432 602632214
42	20.6	73.6	516	12	BM159980	BM159980 EST562503
43	20.6	73.6	606	13	BM159980	BM159980 EST562503
44	20.6	73.6	616	12	BG064533	BG064533 H3020H02-
45	20.6	73.6	632	12	BG077948	BG077948 H3020H02-

ALIGNMENTS

RESULT 1
BH009254
LOCUS ef26a02.x1 TO1000 Brassica oleracea genomic clone ef26a02 5', DNA
DEFINITION
ACCESSION BH009254
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
Katarl,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J., Ballia
,V., Bell,M., Cunnitus,D.M., King,L., Kirchoff,K., Kuit,R., Miller
,B., Nascento,L., Preston,R., Rodriguez,S., Santos,L., Shah,R.,
Vill,M.D., Zutavern,T., Bal,H., Dedhia,N. and McCombie,W.R.
Whole Genome Shotgun Reads from Brassica oleracea
Unpublished (2001)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@csbl.org
Plate: ef26 row: a column: 02
Seq primer: -21ttwduniv

```

Class: shotgun
High quality sequence stop: 613.
Location/Qualifiers
1. 613
/organism="Brassica oleracea"
/db_xref="taxon:3712"
/clone="ef26a02"
/note="Vector: M13 for .x reads, pZero-2 for .b and .g
reads; Site:1: EcoRV; DNA prepared as whole genome shotgun
library from young, green leaves. May contain some plasmid
DNAs. DNA provided by Dr. Tom Osborn, University of
Wisconsin-Madison, Department of Agronomy."
BASE COUNT      175 a      121 c      128 g      189 t
ORIGIN

Query Match      82.9%; Score 23.2; DB 17; Length 613;
Best Local Similarity 89.3%; Pred.No. 9.6e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

v
1 AAGAGAAAAAGATGGCAAGATATTCAA 28
||||| ||||| ||||| ||||| |||||
yb 106 AAGAGAAAGAGATGGCAAGACTTCAA 133

RESULT 2
BH532191      707 bp      DNA      linear      GSS 14-DEC-2001
LOCUS      BOPPX68TF BOPP Brassica oleracea genomic clone BOPPX68, DNA
DEFINITION      sequence.
ACCESSION      BH532191
VERSION      BH532191.1 GI:17753725
KEYWORDS      GSS.
ORGANISM      Brassica oleracea.
                Brassica oleracea.
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 707)
AUTHORS      Town,C.D., Van Aken,S., Uteerback,T. and Fraser,C.M.
TITLE      Whole genome shotgun sequencing of Brassica oleracea
JOURNAL      Unpublished (2001)
COMMENT      Other-GSSs: BOPPX68TR
                Contact: Chris Town
                TIGR
                9712 Medical Center Drive, Rockville, MD 20850, USA.
                Tel: 301-838-3523
                Fax: 301-838-0208
                Email: cdtown@tigr.org
                DNA is from a doubled haploid provided by Tom Osborn.
                Seq primer: TF
                Class: sheared ends.
                Location/Qualifiers
                1. 707
                /organism="Brassica oleracea"
                /strain="TO1000DH3"
                /db_xref="taxon:3712"
                /clone="BOPPX68"
                /clone_1db="BOPG"
                /note="Vector: pHOST1; Site_1: BstXI; 2-3 kb sheared
                genomic DNA inserted into pOST1 using BstXI linkers"
BASE COUNT      187 a      139 c      147 g      234 t
ORIGIN

Query Match      82.9%; Score 23.2; DB 17; Length 707;
Best Local Similarity 89.3%; Pred.No. 9.4e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 AAGAGAAAAAGATGGCAAGATATTCAA 28
||||| ||||| ||||| ||||| |||||
yb 37 AAGAGAAAGAGATGGCAAGACTTCAA 64

```

	RESULT_3	CNS06tyol/c	CNS06tyol	921 bp	DNA	linear	GSS 06-JUL-2001
	LOCUS		T7 end of clone AY0AA011H08 of library AY0A from strain CBS 6340				
	DEFINITION		of Kluyveromyces thermotolerans , genomic survey sequence.				
	ACCESSION		AL421343				
	VERSION		AL421343.1				
	KEYWORDS		GSS.				
SOURCE		Kluyveromyces thermotolerans . Kluyveromyces thermotolerans . Fukayama, Fungi; Ascomycota; Saccharomycetia; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces. 1 (bases 1 to 921)					
REFERENCE	AUTHORS	Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bojotin-Fukuhara,,M., Bon,E., Broclicier,P., Casaregola,S., de-Montigny,B., Dujon,B., Durieux,P., Lepingle,A., Lorente,B., Malpertuy,A., Neugeglise,C., Ozler-Kalogeropoulos,O., Pollier,S., Saurin,W., Tekala,F., Toffano-Nicche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.J.					
TITLE		Genomic exploration of the hemiascomycetous yeasts : 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000) 2 (bases 1 to 921) Malpertuy,A., Loirent,e,B., Blandin,G., Artigue,nave,F., Winck(er),P. and Dujon,B.					
JOURNAL	MEDLINE	Genomic exploration of the hemiascomycetous yeasts : 10. Kluyveromyces thermotolerans FEBS Lett. 487 (1), 61-65 (2000) 20584720 1152876 1152876					
PUBMED							
REFERENCE	AUTHORS	Genoscope - Centre National de Sequencage, Direct Submission Submitted (08-SEP-2000) Genoscope - Centre National de Sequeucage, 2 rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : sequest@genoscope.cns.fr Web : www.genoscope.cns.fr) This GSS Is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert. Location/Qualifiers 1..921 /oranism="Kluyveromyces thermotolerans" /strain="CBS 6340" /db_xref="taxon:4916" /clone="AY0AA011H08" /clone_1lb="AT0AA" /note="end : 77" <18...>329 /note="similar to Saccharomyces cerevisiae ORF YDL015c [similarity to rat synaptic glycoprotein SC2] " /evidence=not experimental complement(<426...>919) /note="similar to Saccharomyces cerevisiae ORF YDL017w [CDC? ; protein kinase] 1 putative frameshift(s)" /evidence=noexperimental]					
BASE COUNT		237 a 212 c 189 g 278 t 5 others					
ORIGIN							
Query Match		82.9% Score 23.2 DB 17 Length 921:					
Match Local Similarity		89.3% Prod No. 9e+02;					
Matches 25 Conservative		0 Mismatches 3 Indels 0 Gaps 0:					

```

Db      240 AAGAAAGACAGCGCAATATATTCAA 213
||||| ||||| ||||| ||||| |||||
RESULT 4
LOCUS   AM255568/c                      618 bp  mRNA  linear  EST 23-AUG-2000
DEFINITION M604 peppermint glandular trichome Mentha x piperita cDNA, mRNA
ACCESSION AM255568
VERSION   AM255568.1  GI:7244820
KEYWORDS EST.
SOURCE    peppermint.
ORGANISM  Mentha x piperita
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Asteridae; euasterids I; Lamiales; Lamiaceae; Mentha.
REFERENCE
AUTHORS  Lange,B.M., Wildung,M.R., Stauber,E.J., Sanchez,C., Pouchnik,D. and
          Croteau,R.
TITLE     Probing essential oil biosynthesis and secretion by functional
          evaluation of expressed sequence tags from mint glandular trichomes
JOURNAL  Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2934-2939 (2000)
COMMENT   Contact: lange, B.M.
          Institute of Biological Chemistry/Washington State University
          Pullman, WA
          Email: lange-m@mail.wsu.edu.
          Location/Qualifiers
            1..618
              /organism="Mentha x piperita"
              /cultivar="Black Mitcham"
              /db_xref="taxon:34256"
              /clone_1lb="peppermint glandular trichome"
              /rname_type="petalate glandular trichomes"
              /cell_type="secretory"
              /note="Vector: lambda ZAP11"
BASE COUNT  182 a 129 c 120 g 187 t
ORIGIN
Query Match      81.4%; Score 22.8; DB 10; Length 618;
Best Local Similarity 92.3%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 AAGAAAAAGATGGCAAGATATTC 26
||||| ||||| ||||| ||||| |||||
Db      552 AAGAAAAAGATGGCAAGATATTC 527

RESULT 5
LOCUS   AQ283551                      360 bp  DNA  linear  GSS 27-APR-1999
DEFINITION RPC11-77B19.TV RPC1-11 Homo sapiens genomic clone RPC1-11-77B19,
          DNA sequence.
ACCESSION AQ283551
VERSION   AQ283551.1  GI:3909946
KEYWORDS GSS.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS  Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
          Berry,K., Granger,D., Sub,E., Wible,C., de Jong,P. and Venter,J.C.
          Use of human BAC End Sequences for Sequence-Ready Map Building
          Unpublished (1998)
JOURNAL  Other_GSSs: RPC11-77B19.TV
COMMENT   Contact: Mark Adams
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0200
          Fax: 301 838 0208

```

```

Email: mdadams@tigr.org
Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC end.

FEATURES
source      Location/Qualifiers
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              /organism="Homo sapiens"
              /db_xref="GDB:7529226"
              /db_xref="taxon:9606"
              /clone="RPC1-11-77B19"
              /clone_1lb="RPC1-11"
              /sex="Male"
              /cell_type="lymphocytes"
              /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
              RPC111 Human Male BAC library"
BASE COUNT  156 a 49 c 58 g 97 t
ORIGIN
Query Match      79.3%; Score 22.2; DB 17; Length 360;
Best Local Similarity 86.9%; Pred. No. 2.1e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 AAGAAAAAGATGGCAAGATATTC 28
||||| ||||| ||||| ||||| |||||
Db      211 AAGAAAAATATCGCAAGCAATTC 237

RESULT 6
LOCUS   BM875833/c                      353 bp  mRNA  linear  EST 07-MAR-2002
DEFINITION iB6d03.x1 Kaestner ngn3 - - subtracted Mus musculus cDNA 3', mRNA
          sequence.
ACCESSION BM875833
VERSION   BM875833.1  GI:19243499
KEYWORDS EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
           Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Eukaryota; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.
           1 (bases 1 to 353)
REFERENCE
AUTHORS  Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
          Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
          Hillier,L., Marra,M., Page,D., Wylie,T., Martin,J., Hirstain,A.,
          Schmitt,A., Rhising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
          /M., Gibbons,M., McCann,R., Cole,K., Tsagarisvili,I., Williams,T.,
          Jackson,X. and Bowers,Y.
           Endocrine Pancreas Consortium
           Unpublished (2000)
           Other_ESTs: iB6d03.y1
JOURNAL  Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
           Endocrine Pancreas Consortium
           Harvard University, Howard Hughes Medical Institute
           Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
           MA 02138
           Tel: 617-495-1812
           Fax: 617-495-8557
           Email: dmelton@biohp.harvard.edu
           Mammals was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
           2000) Library was constructed by Catherine Lee DNA sequencing by:
           Washington University Genome Sequencing Center For information on
           obtaining a clone please contact: Dr. Marie Searce
           (msearce@mail.med.upenn.edu)
           Seq primer: -400p from Gibco
           High quality sequence stop: 343.
           Location/Qualifiers
            1..353
              /organism="Mus musculus"
              /strain="129/Sv x C57BL"

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```

FEATURES
  source
    POLYA-NO.
    Location/Qualifiers
      1..507
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone_image="420214"
        /clone_lib="Soares mouse embryo NDBE13.5 14.5"
        /sex="unknown"
        /tissue_type="embryo"
        /dev_stage="13.5-14.5dpc total fetus"
        /lab_host="DH10B"
        /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACATCTGAGATGGAGCGCGCGCAATTTTATTTTATTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Benito Soares and
M.Fatima Bonaldo."
BASE COUNT      146 a      128 c      147 g      85 t      1 others
ORIGIN

Query Match      77.1%; Score 21.6; DB 9; Length 507;
Best Local Similarity 85.7%; Pred. No. 3.1e+03;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 AAGCAAAAAGATGCGCAAGATATTCAA 28
Db      319 AAGCAAAAAGAGAGCAGATGATCAA 346

RESULT 11
LOCUS      A2216057      589 bp      DNA      linear      GSS 09-JUN-2000
DEFINITION      Sheared DNA-56F11.TR Sheared DNA Trypanosoma brucei genomic clone
ACCESSION      A2216057
VERSION      A2216057.1 GI:8433857
KEYWORDS      GSS.
SOURCE      Trypanosoma brucei.
ORGANISM      Trypanosoma brucei.
      Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
      Trypanosoma.
      1 (bases 1 to 589)
      El-Sayed,N., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
      Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
      Fraser,C. and Adams,M.
      Determination of clone end sequences from Trypanosoma brucei gutat
      10.1 sheared DNA library
      Unpublished (1999)
      Other_GSS: Sheared DNA-56F11.TF
      Contact: Najib M. El-Sayed
      Department of Eukaryotic Genomics
      The Institute for Genomic Research
      9712 Medical Center Dr., Rockville, MD 20850, USA
      Tel: 301 838 0200
      Fax: 301 838 0208
      Email: nelsayed@tigr.org
      Clones are derived from the Trypanosoma brucei gutat 10.1 sheared
      DNA library constructed at TIGR. Clones will be available for
      distribution through Research Genetics, Alabama, USA. Sheared DNA
      end sequences search page: http://www.tigr.org/tldb/mdb/tldb/.
      Seq primer: M13-Reverse
      Class: Shotgun.
FEATURES
  source
    Location/Qualifiers
      1..589
        /organism="Trypanosoma brucei"
        /strain="TREU927/4 gutat 10.1"

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      /db_xref="taxon:5691"
      /clone="Sheared DNA-56F11"
      /clone_lib="Sheared DNA"
      /note="Vector: pUC18; Site_1: SmaI; Constructed at The
      Institute for Genomic Research (TIGR), Rockville, MD.
      Trypanosoma brucei (TREU927/4 gutat 10.1) was mechanically
      sheared to give a tight size distribution (approx 2 kb).
      The v + i method used for the library construction is
      described in detail in Smith, H.O. and Venter, J.C.
      (Making small insert libraries for whole genome shotgun
      sequencing projects. In Genome Sequencing: A Practical
      Approach, eds. M. Vaudin and B. Barrell, Oxford University
      Press, 1999)."
BASE COUNT      152 a      101 c      108 g      228 t
ORIGIN

Query Match      77.1%; Score 21.6; DB 17; Length 589;
Best Local Similarity 85.7%; Pred. No. 3e+03;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 AAGCAAAAAGATGCGCAAGATATTCAA 28
Db      337 AAAAAAAGATGATMAAGATATCAA 310

RESULT 12
LOCUS      AQ487311      621 bp      DNA      linear      GSS 24-APR-1999
DEFINITION      RPCI-11-245E21.TV RPCI-11 Homo sapiens genomic clone RPCI-11-245E21
      , DNA sequence.
ACCESSION      AQ487311
VERSION      AQ487311.1 GI:4673185
KEYWORDS      GSS.
SOURCE      human.
ORGANISM      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      1 (bases 1 to 621)
      Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and Venter
      ,J.C.
      Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
      Map Building
      Unpublished (1997)
      Other_GSS: RPCI-11-245E21.TJ
      Contact: Shaying Zhao, William Niernan, Mark Adams
      Department of Eukaryotic Genomics
      The Institute for Genomic Research
      9712 Medical Center Dr., Rockville, MD 20850
      Tel: 301 838 0200
      Fax: 301 838 0208
      Email: hbe@tigr.org
      Clones are derived from the human BAC library RPCI-11. For BAC
      library availability, please contact Pieter de Jong
      (pieter@dejong.med.buffalo.edu). Clones may be purchased from
      BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
      Research Genet. cs (info@resgen.com). BAC end search page:
      http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
      Seq primer: T7
      Class: BAC ends.
FEATURES
  source
    Location/Qualifiers
      1..621
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        /db_xref="GDB:7593812"
        /db_xref="taxon:9606"
        /clone="RPCI-11-245E21"
        /clone_lib="RPCI-11"
        /sex="Male"
        /cell_type="Lymphocytes"
        /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
      RPC11 Human Male BAC Library"
BASE COUNT      175 a      112 c      105 g      229 t
ORIGIN

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	Query Match	77.1%	Score 21.6:	DB 17:	Length 621;	
	Best Local Similarity	85.7%	Pred. No. 3e+03;			
	Matches 24; Conservative	0;	Mismatches	4;	Indels	0;
OY	1 AAGGAAAAAGATGGCAAAATATTCTA 28 AAAAAAAAACAGACGATTAATTTCAA 463					
Db	490 AAGGAAAAAGATGGCAAAATATTCTA 463					
LOCUS	BB642313					
DEFINITION	BB642313 RIKEN full-length enriched, adult retina Mus musculus cDNA clone A930010A15 5', mRNA sequence.					
VERSION	BB642313					
KEYWORDS	EST.					
SOURCE	BB642313.1 GI:16477263					
ORGANISM	house mouse. Mus musculus					
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia; Sciurognathi: Muridae; Murinae; Mus. 1 (bases 1 to 636)					
AUTHORS	Arakawa,T., Carinici,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sodabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.					
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001)					
JOURNAL	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research(Riken) 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.					
COMMENT	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10). 1617-1630 (2000) Wagci,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanishi,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11). 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2). 281-289 (2001) Kondo,S., Shingawa,A., Saito,T., Kiyoawa,H., Yamaneke,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues. Location/Qualifiers 1..636 /organism="Mus musculus" /db_xref="taxon:10090" /clone_id="A930010A15" /clone_lib="RIKEN full-length enriched, adult retina" /tissue_type="retina"					
FEATURES						
SOURCE						

```

/deef_stage="adult"
/lab_host="DHI08"
/note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer 15'
GAGCAGAGAGAGCATCCACAGACGCTCTTTTCTTTTCTTTTCTTTVN 3', cDNA was
transcribed by using trehalase thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence 15'GAGCAGAGAGATCTCCGACGTTATTTAAATTAATCCCCCCCC
3'. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. -Retina RNA was provided by Stefano Gustlinich,
Department of Neurobiology, Harvard Medical School, 220
Longwood Ave., Boston, MA02115, USA, whose assistance we
gratefully acknowledge."

BASE COUNT      195 a      130 c      159 g      152 t

ORIGIN
Query Match      77.1%; Score 21.6; DB 10; Length 636;
Best Local Similarity 85.7%; Pred. No. 2.9e+03;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      1 AAGGAAAAAGATGGCAAGAATTTCAA 28
Db      331 AAAAAAAAAGGTGGCAATAATTTAA 358
      111 111111 111111 11111 11
      11 111111 111111 11111 11

RESULT 14
LOCUS      BB660787      639 bp      mRNA      linear      EST 26-OCT-2001
DEFINITION BB660787 RIKEN full-length enriched, 0 day neonate kidney Mus
            musculus cDNA clone D630005H02 5', mRNA sequence.
ACCESSION  BB660787
VERSION    BB660787.1 GI:16494567
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 639)
Arakawa,T., Carolini,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okada,
M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Tsurumi-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: http://genome-gsc.riken.go.jp/
Carlini,P., Shibata,Y., Hayashi,N., Sugahara,Y., Shibata,K., Itoh
M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagii,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,F.,
Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and

```

Hayashizaki, Y.
 RIKEN Integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
 , Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
 , K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human genome sequences. Mamm. Genome, 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 e mouse tissues.

FEATURES

source

location/Qualifiers

1..639
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="D63005H02"
 /clone.lib="RIKEN full-length enriched, 0 day neonate
 kidney"
 /tissue_type="kidney"
 /dev_stage="0 day neonate"
 /lab_host="DH10B"
 /note="Site_1: SalI; Site_2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer 15'
 GAGACAGACAGCCGCCACACCTCGAGTTTCTTTTCTTTTNN 3', cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence 15'
 CAGACAGAGATTTCGACTTATTATAATTATCCCCCCCCCC 3'. cDNA
 was cleaved with BamHI and XhoI. Vector: a modified
 pBluescript KS(+) after bulk excision from lambda FLC I."

BASE COUNT

187 a 155 c 131 g 166 t

ORIGIN

Query Match 77.1%; Score 21.6; DB 10; Length 639;
 Best Local Similarity 85.7%; Pred. No. 2.9e+03;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 AAGAGAAAAAGATGGCAAGATATTCAA 28
 ||| ||||| ||||| ||||| ||||| ||
 18 AAAAAAAAAAGCTGCCAATATTATAA 45

RESULT 15

BH029119

685 bp DNA linear GSS 17-JUL-2001

LOCUS

RPCI-24-336F4.TV RPCI-24 Mus musculus genomic clone RPCI-24-336F4,
 DNA sequence.

ACCESSION

BH029119

VERSION

BH029119.1 GI:14796446

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 685)
 Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akimret, B., Levins, M.,
 Tsegaye, G., Goert, K., Kroll, M., Shvartsbeyn, A., Gebregorgis, E.,
 Russell, D., de Jong, P. and Fraser, C. M.

AUTHORS

Mouse BAC End Sequences from Library RPCI-24

TITLE

Unpublished (1999)

JOURNAL

Other-GSS: RPCI-24-336F4.TV

COMMENT

Other-GSS: RPCI-24-336F4.TV

Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@ligr.org
 Clones are derived from the mouse BAC library RPCI-24. For BAC
 library availability, please contact Pieter de Jong
 (piet@ligr.org). Clones may be purchased from BACPAC
 Resources (<http://www.chori.org/bacpac/orderingframe.html>). BAC end
 page: http://www.ligr.org/lbd/bac-ends/mouse/bac_end_intro.html
 plate: 336 row: F column: 4
 Seq primer: 17
 Class: BAC ends.

FEATURES

source

location/Qualifiers

1..685
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-24-336F4"
 /clone.lib="RPCI-24"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /note="Vector: pTARBAC1; Site_1: BamHI; Site_2: BamHI;
 RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
 library was cloned in the pTARBAC1 cloning vector at the
 BamHI sites using MboI partially digested male C57BL/6J
 DNA."

BASE COUNT

283 a 159 c 93 g 150 t

ORIGIN

Query Match 77.1%; Score 21.6; DB 17; Length 685;
 Best Local Similarity 85.7%; Pred. No. 2.9e+03;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

0Y 1 AAGAGAAAAAGATGGCAAGATATTCAA 28
 ||| ||||| ||||| ||||| ||||| ||
 DB 221 AAGAGAAAAAAATGCAAAATATTCAA 248

Search completed: December 10, 2002, 22:50:05
 Job time: 1440.66 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 : Search time 717.832 Seconds

(without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579A-19

Perfect score: 14

Sequence: 1 gaaggtgcttac 14

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	14	100.0	134	17	AZ506708 1M0348C03
C 2	14	100.0	215	9	AV221833 AV221833
C 3	14	100.0	266	17	AZ906716 RPCI-24-1
C 4	14	100.0	383	9	AI699442 DKFp6860
C 5	14	100.0	404	10	BE457319 US49910.Y
C 6	14	100.0	417	14	BQ457284 ke37b11.Y

7	14	100.0	457	9	AL368921
C 8	14	100.0	615	17	AQ930007
C 9	14	100.0	617	17	AZ103489 RPCI-23-2
C 10	14	100.0	649	17	AZ396567 1M0161K10
C 11	14	100.0	666	12	BC351941
C 12	14	100.0	746	12	BC753057
C 13	14	100.0	752	13	BI180700
C 14	14	100.0	755	17	CNS02819
C 15	14	100.0	776	14	BQ137473
C 16	14	100.0	834	17	BH271990
C 17	13.2	94.3	761	17	CNS01KR1
C 18	13	92.9	170	13	BI798912
C 19	13	92.9	194	14	BO908524
C 20	13	92.9	203	17	AQ067864
C 21	13	92.9	215	17	AZ603386
C 22	13	92.9	219	13	BI810470
C 23	13	92.9	226	10	BE158465
C 24	13	92.9	226	10	BB075983
C 25	13	92.9	242	13	BI807592
C 26	13	92.9	254	17	AQ096625
C 27	13	92.9	265	12	BC652767
C 28	13	92.9	277	17	AZ739865
C 29	13	92.9	283	10	BH054421
C 30	13	92.9	286	10	BB405195
C 31	13	92.9	292	9	AI438086
C 32	13	92.9	297	13	BM421408
C 33	13	92.9	302	17	AZ117887
C 34	13	92.9	308	10	AA936263
C 35	13	92.9	312	10	BB400372
C 36	13	92.9	315	10	BB491091
C 37	13	92.9	316	17	AZ072871 RPCI-23-4
C 38	13	92.9	325	12	BE818340
C 39	13	92.9	333	9	AA607080
C 40	13	92.9	333	14	BO517712
C 41	13	92.9	334	9	AA664420
C 42	13	92.9	336	10	AV743946
C 43	13	92.9	336	10	AW875934
C 44	13	92.9	354	10	AW875648
C 45	13	92.9	356	10	BE230109

ALIGNMENTS

RESULT 1	AZ506708/c	134 bp	DNA	linear	GSS 05-OCT-2000
LOCUS	1M0348C03F	Mouse 10kb plasmid	UUGCM library	Mus musculus	genomic
DEFINITION	clone UUGCM0348C03 F, DNA sequence.				
ACCESSION	AZ506708				
VERSION	AZ506708.1	GI:10688024			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb				
JOURNAL	Plasmid Inserts				
COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00				

Plate: 0348 row: C column: 03
 Seq primer: CGTTCGTAACGACGCGCAGT
 Class: Plasmid ends
 High quality sequence stop: 134.

FEATURES

source

1. 134
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 /clone_1ib="Mouse 10kb plasmid UUC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6j (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b/AH129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 36 a 31 c 28 g 39 t
 ORIGIN

Query Match 100.0%; Score 14; DB 17; Length 134;
 Best Local Similarity 100.0%; Pred. No. 9.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTGCTTAC 14
 Db 59 GAAGGTGCTGCTTAC 46

RESULT 2 215 bp mRNA linear EST 14-NOV-2001
 AV221833 RIKEN full-length enriched, adult male brain Mus musculus
 LOCUS cDNA clone 3526402016 3' similar to U58280 Mus musculus second
 DEFINITION largest subunit of RNA polymerase I (RP42) mRNA, mRNA sequence.

AV221833 GI:6171010
 AV221833
 AV221833.1 GI:6171010
 EST.
 house mouse.
 Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 215)
 Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
 Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
 Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai
 C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
 Owa, C., Ozawa, Y., Saito, H., Sano, M., Saito, K., Shibata, K., Shibata,
 Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H.,
 Suzuki, H., Takahashi, F., Tateno, M., Tomioka, N., Tsunoda, Y.,
 Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,
 Yoshiki, A., Yoshino, M., Yamamoto, M., and Hayashizaki, Y.

TITLE RIKEN Mouse ESTs (Kono, H., et al. 1999)

JOURNAL Unpublished (1999)

COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-resgsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
 Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki,
 Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3453-3460 (1998)
 Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
 Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES

source

1. 215
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6j"
 /db_xref="taxon:10090"
 /clone="3526402016"
 /clone_1ib="RIKEN full-length enriched, adult male brain"
 /sex="male"
 /tissue_type="brain"
 /dev_stage="adult"
 /lab_host="DH10B"

/note="Site_1: SalI; Site_2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGATCCAGACCTCTTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence 15'
 GAGAGAGATTCGAGTTTAATTAATTAATCCCCCCCC 3'}. cDNA
 was cloned into the XhoI and BamHI sites. Vector: a
 modified pBluescript KS(+) after bulk excision from Lambda
 phage 1."

BASE COUNT 58 a 36 c 49 g 72 t
 ORIGIN

Query Match 100.0%; Score 14; DB 9; Length 215;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTGCTTAC 14
 Db 12 GAAGGTGCTGCTTAC 25

RESULT 3 266 bp DNA linear GSS 05-MAR-2001
 AV2906716 RPCI-24-164B11.TV RPCI-24 Mus musculus genomic clone RPCI-24-164B11
 LOCUS , DNA sequence.
 DEFINITION

AV2906716 GI:13225661
 AV2906716.1 GI:13225661
 GSS.
 house mouse.
 Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 266)

AUTHORS

Zhao, S., Niemman, M., Malek, J., Shatsman, S., Aktinret, B., Levins, M.,
 Tesgaye, G., Geer, K., Kroll, M., Shvartsbeyn, A., Gebregorgis, E.,
 Russell, D., de Jong, P., and Fraser, C.M.
 Mouse BAC End Sequences from Library RPCI-24
 Unpublished (1999)
 Other GSSs: RPCI-24-164B11.TJ

JOURNAL

Contact: Shaying Zhao

Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC
 library availability, please contact Pieter de Jong
 (pdejong@mail.cho.org). Clones may be purchased from BACPAC
 Resources (<http://www.choi.org/bacpac/orderingframe.html>). BAC end
 page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
 Plate: 164 row: B column: 11
 Seq primer: 47
 Class: BAC ends.

FEATURES

Location/Qualifiers

1..266
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-24-164B11"
 /clone_lib="RPCI-24"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /note="Vector: pTRABAC1; Site_1: BamHI; Site_2: BamHI;
 RPCI-24 Mouse BAC library produced by Pieter de Jong. The
 library was cloned in the pTRABAC1 cloning vector at the
 BamHI sites using MboI partially digested male C57BL/6J
 DNA."

BASE COUNT 56 a 48 c 84 g 78 t
 ORIGIN

Query Match

Best Local Similarity 100.0%; Score 14; DB 17; Length 266;
 Pred. No. 1.2e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14
 |||||||

Db 60 GAAGTGTGCTTAC 73

RESULT 4

1699442

DEFINITION DKFZp68601113.F1 686 (synonym: hicc3) Homo sapiens cDNA clone
 DKFZp68601113.5', mRNA sequence.
 ACCESSION AL699442
 VERSION AL699442.1 GI:19619982
 KEYWORDS EST.

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Ottenwaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Weill, B. and
 Wiemann, S.
 EST (Ottenwaelder, B., Obermaier, B., Mewes, H.W., Weill, B. and Wiemann
 , S.)

TITLE

Unpublished (2001)

JOURNAL

Contact: Ottenwaelder B

COMMENT

MIPS

Am Kioferspitz 18a D-82152 Martinsried, Germany
 This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ). Email: s.wiemann@dkfz-heidelberg.de
 Sequenced by Medigenomix (Martinsried/Germany) within the cDNA
 sequencing consortium of the German Genome Project. No sl sequence

available.

This clone (DKFZp68601113) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin - Charlothenburg, GERMANY; Email: clonerzpd.de.

FEATURES

source

Location/Qualifiers

1..383
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="DKFZp68601113"
 /clone_lib="686 (synonym: hicc3)"
 /issue_type="human skeletal muscle"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Vector: pTRIPlex2; Site_1: SfiIA; Site_2: SfiIB;
 cDNA-collection"

BASE COUNT 125 a 60 c 104 g 94 t
 ORIGIN

Query Match

Best Local Similarity 100.0%; Score 14; DB 9; Length 383;
 Pred. No. 1.5e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14
 |||||||

Db 285 GAAGTGTGCTTAC 298

RESULT 5

BE457319/c

LOCUS BE457319 404 bp mRNA linear EST 26-JUL-2000
 DEFINITION us49g10.y1 Perkins LRH Mus musculus cDNA clone IMAGE:3215778.5',
 mRNA sequence.
 ACCESSION BE457319
 VERSION BE457319.1 GI:9479333
 KEYWORDS EST.

SOURCE

house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 404)
 Marra, M., Hillier, L., Kucaba, T., Martini, J., Beck, C., Wylie, T.,
 Underwood, K., Stepien, M., Theising, B., Allen, M., Hovers, Y., Nelson
 B., Waller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
 E., Kohn, S., Shin, T., Jackson, V., Cardenas, M., McCann, R.,
 Waterston, R. and Wilson, R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)

TITLE

Contact: Marra, M/WashU-NCI Mouse EST Project 1999

JOURNAL

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LBNL; contact the
 IMAGE Consortium (infoimage.llnl.gov) for further information.
 MGI:1065926

Seq primer: -400P from Gibco
 High quality sequence stop: 347.
 Location/Qualifiers

FEATURES

source

Location/Qualifiers

1..404
 /organism="Mus musculus"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="IMAGE:3215778"
 /clone_lib="Perkins LRH"
 /sex="female"
 /tissue_type="primary sorted bone marrow cells"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /note="Vector: pZL1; Site_1: Sall; Site_2: EagI; cDNA made
 by oligo-dT priming. Library amplified by stretch PCR.
 Subtraction method: Bonaldo, et al., Genome Research
 6:791. Library constructed by Dr. Archibald Perkins (Yale

ACCESSION A0930007
 VERSION A0930007.1 GI:6618937
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 615)
 Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.M.
 Mouse BAC End Sequences from library RPCI-23
 Unpublished (1999)
 Other-GSSs: RPCI-23-283F20.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhaost@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pietor de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 283 row: F column: 20
 Seq primer: SP6
 Class: BAC ends.
 Location/Qualifiers
 1..615
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-283F20"
 /clone_1lb="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1; EcoRI: Site 2; EcoRI: Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 171 a 148 c 126 g 170 t
 r t c g a
 Query Match 100.0%; Score 14; DB 17; Length 615;
 Best Local Similarity 100.0%; Pred. NO. 1.8e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GAAGCTGTCCTTAC 14
 ||||||||||||
 Db 360 GAAGGTGTCCTTAC 347
 RESULT 9
 AZ103489/c 617 bp DNA linear GSS 09-MAY-2000
 LOCUS RPCI-23-2308.TJ RPCI-23 Mus musculus genomic clone RPCI-23-2308,
 DEFINITION DNA sequence.
 ACCESSION AZ103489
 VERSION AZ103489.1 GI:7756547
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 617)
 Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatsman, S., Akinret

TITLE
 JOURNAL
 COMMENT
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other-GSSs: RPCI-23-2308.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhaost@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pietor de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 23 row: 0 column: 8
 Seq primer: SP6
 Class: BAC ends.
 Location/Qualifiers
 1..617
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-2308"
 /clone_1lb="RPCI-2"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1; EcoRI: Site 2; EcoRI: Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 166 a 153 c 124 g 174 t
 r t c g a
 Query Match 100.0%; Score 14; DB 17; Length 617;
 Best Local Similarity 100.0%; Pred. NO. 1.8e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GAAGCTGTCCTTAC 14
 ||||||||||||
 Db 343 GAAGGTGTCCTTAC 330
 RESULT 10
 AZ396567 649 bp DNA linear GSS 03-OCT-2000
 LOCUS IM0161K10F Mouse 10kb plasmid UGCCIM library Mus musculus genomic
 DEFINITION clone UGCCIM0161K10 F, DNA sequence.
 ACCESSION AZ396567
 VERSION AZ396567.1 GI:10511639
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 649)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0161 row: K column: 10
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 649.
location/Qualifiers

FEATURES
source
1..649
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0161K10"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (911473211419b|AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
216 a 129 c 93 g 211 t

ORIGIN

Query Match 100.0%; Score 14; DB 17; Length 649;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGCTTAC 14
|||||

Db 274 GAAGCTGCTTAC 287

30UT 11
.351941
LOCUS 666 bp mRNA linear EST 01-MAR-2001
DEFINITION 134G06 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA
sequence.
ACCESSION BG351941
VERSION BG351941
KEYWORDS EST.
SOURCE Solanum tuberosum
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 666)
Nielsen, K.L., Crookshanks, M., Emmersen, J. and Welinder, K.G.
EST-sequencing of mature potato tuber (Var. Kuras)
Unpublished (2000)
Contact: Karen G. Welinder
Institut for Biotechnology
Aalborg Universitet
Sohnsgaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.auc.dk

Sequenced from the 5' end.
High quality sequence stop: 666
POLYA=NO.
Location/Qualifiers

FEATURES
source
1..666
/organism="Solanum tuberosum"
/cultivar="Field grown Kuras"
/db_xref="taxon:4113"
/clone_lib="Mature tuber lambda ZAP"
/tissue_type="tuber"
/note="vector: lambda ZAP"
location/Qualifiers

BASE COUNT 189 a 97 c 184 g 196 t

ORIGIN

Query Match 100.0%; Score 14; DB 12; Length 666;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGCTTAC 14
|||||

Db 77 GAAGCTGCTTAC 90

RESULT 12
BG753057 746 bp mRNA linear EST 15-MAY-2001
LOCUS 602732326F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4875606 5',
DEFINITION mRNA sequence.
ACCESSION BG753057
VERSION BG753057.1 GI:14063710
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 746)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: MGC Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at:
http://image.llnl.gov
Plate: LCM1757 row: d column: 07
High quality sequence stop: 742.
location/Qualifiers

FEATURES
source
1..746
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:4875606"
/clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library.!"

BASE COUNT 223 a 159 c 191 g 173 t

ORIGIN

Query Match 100.0%; Score 14; DB 12; Length 746;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

VERSION	AL185382.1	GI:7823486
KEYWORDS	GSS; genome survey sequence.	
SOURCE	Tetraodon nigroviridis.	
ORGANISM	Tetraodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euleleostei; Neoleleostei; Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.	
REFERENCE	1 (bases 1 to 765)	
AUTHORS	Roeck-Crollius,H., Jallion,O., Dasilva,C., Bonnaue,I., Fisher,C., Bernot,A., Pizames,C., Winkler,P., Brotlier,P., Quetier,F., Saurin,W. and Weissbach,J. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence	
TITLE	Unpublished	
JOURNAL	2 (bases 1 to 765)	
REFERENCE	Roeck-Crollius,H., Jallion,O., Dasilva,C., Pizames,C., Fisher,C., Bonnaue,I., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis	
TITLE	Unpublished	
JOURNAL	3 (bases 1 to 765)	
REFERENCE	Genoscope.	
AUTHORS	Direct Submission	
TITLE	Submitted (12-APR-2000)	
JOURNAL	This sequence is a single read and was generated as part of a large scale clone-and sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon .	
COMMENT	Location/Qualifiers	
FEATURES	source	
	1..765	/organism="Tetraodon nigroviridis"
	/db_xref="taxon:99883"	
	/clone="244A19"	
	/clone_lib="G"	
	/note="Genoscope sequence ID : COAG244AA10SP1-end :	
	PUC-Orl"	
BASE COUNT	224 a 185 c 177 g 178 t	1 others
ORIGIN		
	Query Match	100.0%; Score 14; DB 17; Length 765;
	Best Local Similarity	100.0%; Pred. No. 2e+03;
	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 GAAGCTGCCTTAC 14	
DB	503 GAAGGTGTCTTAC 516	
RESULT 15		
LOCUS	BO137473	776 bp mRNA linear EST 23-APR-2002
DEFINITION	NF012006N1.F1000 Modulated root Medicago truncatula CDNA clone	
ACCESSION	NF012006N 5', mRNA sequence.	
VERSION	BO137473	
KEYWORDS	BO137473.1 GI:20273559	
SOURCE	EST.	
ORGANISM	barrel medic.	
	Medicago truncatula	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;	
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;	
	Medicago.	
REFERENCE	1 (bases 1 to 776)	
AUTHORS	Watson,B.-S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R., Gonzalez,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May, .G.D. and Patwa,N.L. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula modulated root library Unpublished (2000) Contact: Patwa NL Plant Biology Division	
TITLE		
JOURNAL		
COMMENT		

The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7317
Fax: 580 221 7380

Email: nlpaiva@noble.org

Insert length: 776 Std Error: 0.00

Plate: 012 Row: D Column: 06

Seq primer: TCACACAGCAACACGCTATGAC.

FEATURES

Source

1..776

/organism="Medicago truncatula"

/db_xref="taxon:380"

/clone="NF012D06NR"

/clone_id="Nodulated root"

/issue_type="root"

/dev_stage="Pooled developmental"

/note="Vector: lambda Zap; Four-week old Rhizobium

meliloti-inoculated Medicago truncatula roots, containing

a mixture of young and old roots and nodules."

a mixture of young and old roots and nodules."

11 others

BASH COUNT
IGIN

238 a

188 c

177 g

162 t

11 others

Query Match

Best local similarity 100.0%; Score 14; DB 14; Length 776;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTCGCTTAC 14
|||||

Db 366 GAAGGTGCTTAC 353

Search completed: December 10, 2002, 22:49:51
Job time : 722.832 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 ; Search time 455.313 Seconds

(Without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579a-20

Perfect score: 21

Sequence: 1 tttcttcttctctataatg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pin:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	21	100.0	21	6	AX306851	AX306851 Sequence
2	21	100.0	21	6	AX306861	AX306861 Sequence
3	21	100.0	39	6	AX306868	AX306868 Sequence
4	21	100.0	1789	6	E09772	E09772 The base se
5	21	100.0	2007	6	AR089410	AR089410 Sequence
6	21	100.0	2007	6	AR093610	AR093610 Sequence
7	21	100.0	2322	1	SAPAP	Y00688 Staphylococ
8	21	100.0	2322	6	E03736	E03736 DNA sequenc
9	21	100.0	2454	1	SEMECAPB	X52592 S. epiderm
10	21	100.0	2455	6	E09771	E09771 The base se
11	21	100.0	2456	6	SAMECAPB	X52593 S. aureus m
12	21	100.0	2456	6	AX110445	AX110445 Sequence
13	21	100.0	5068	1	SSK1MECA	Y09223 S. sciuri me
14	21	100.0	5596	1	SSK8MECA	Y13096 S. sciuri me
15	21	100.0	6368	1	SSK3MECA2	Y13095 S. sciuri me
16	21	100.0	9047	1	SAMECARL1	Y14051 Staphylococ
17	21	100.0	21777	1	AB063173	AB063173 Staphyloc
18	21	100.0	26090	1	AB063172	AB063172 Staphyloc
19	21	100.0	39332	1	AB033763	AB033763 Staphyloc
20	21	100.0	58237	1	D86934	D86934 Staphylococ
21	21	100.0	68256	1	AB037671	AH037671 Staphyloc
22	21	100.0	290250	1	AP004822	AP004822 Staphyloc
23	21	100.0	298050	1	AP003129	AP003129 Staphyloc
24	21	100.0	349999	9	AC099664	AC099664 Homo sapi
25	20	95.2	157223	9	AC099664	AC099664 Homo sapi
26	20	95.2	183978	2	AC024967	AC024967 Homo sapi
27	19.4	92.4	6684	1	SSK11MECA	AL73994 S. sciuri me
28	19.4	92.4	64986	9	AL499610	AL499610 Human DNA
29	19.4	92.4	74119	2	AC036177	AC036177 Homo sapi
30	19.4	92.4	130110	9	AL731777	AL731777 Human DNA
31	19.4	92.4	132906	2	AC111352	AC111352 Rattus no
32	19.4	92.4	135160	9	AC016894	AC016894 Homo sapi
33	19.4	92.4	135450	9	AC112131	AC112131 Homo sapi
34	19.4	92.4	138245	8	AC027662	AC027662 Oryza sat
35	19.4	92.4	139035	2	AC108917	AC108917 Mus muscu
36	19.4	92.4	141854	2	AC021595	AC021595 Homo sapi
37	19.4	92.4	148517	2	AC011147	AC011147 Homo sapi
38	19.4	92.4	152449	2	AC080175	AC080175 Homo sapi
39	19.4	92.4	154001	9	AC083904	AC083904 Homo sapi
40	19.4	92.4	160174	2	AP005103	AP005103 Oryza sat
41	19.4	92.4	160664	2	AC102419	AC102419 Mus muscu
42	19.4	92.4	171695	9	AC012337	AC012337 Homo sapi
43	19.4	92.4	177964	9	AC016705	AC016705 Homo sapi
44	19.4	92.4	180672	9	AC011451	AC011451 Homo sapi
45	19.4	92.4	186120	2	AC125910	AC125910 Rattus no

ALIGNMENTS

RESULT 1
AX306851
LOCUS AX306851
DEFINITION Sequence 10 from Patent EP1160333.
ACCESSION AX306851
VERSION AX306851.1 GI:17894673
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1
Taya, T., Ishiguro, T. and Saito, J.
Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
Patent: EP 1160333-A 10 05-DEC-2001;
JOURNAL

FEATURES	Tosoh Corporation (JP)
source	Location/Qualifiers
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	/organism="synthetic construct"
	/db_xref="taxon:32630"
	/note="Oligonucleotide capable of binding specifically to
	meca gene or RNA derived from said gene"
BASE COUNT	3 a 3 c 1 g 14 t
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Query Match	100.0%; Score 21; DB 6; Length 21;
Best Local Similarity	100.0%; Pred. No. 1.1e+03;
Matches 21: Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 TTTCTTTTCTCTATTATG 21
Db	1 TTTCTTTTCTCTATTATG 21
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X306861	
XCUS	AX306861 21 bp DNA Linear PAT 14-DEC-2001
DEFINITION	Sequence 20 from Patent EP1160333.
ACCESSION	AX306861
VERSION	AX306861.1 GI:17894683
KEYWORDS	
SOURCE	synthetic construct.
ORGANISM	synthetic construct
REFERENCE	artificial sequences.
AUTHORS	1
TITLE	Taya,T., Ishiguro,T. and Saito,J.
JOURNAL	Oligonucleotides and method for detection of meca gene of
	methicillin-resistant Staphylococcus aureus
	Patent: EP 1160333-A 20 05-DEC-2001;
	Tosoh Corporation (JP)
FEATURES	Location/Qualifiers
source	1..21
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	/note="Primer"
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Best Local Similarity	100.0%; Pred. No. 1.1e+03;
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LOCUS	AX306868 39 bp DNA Linear PAT 14-DEC-2001
DEFINITION	Sequence 27 from Patent EP1160333.
ACCESSION	AX306868
VERSION	AX306868.1 GI:17894690
KEYWORDS	
SOURCE	synthetic construct.
ORGANISM	synthetic construct
REFERENCE	artificial sequences.
AUTHORS	1
TITLE	Taya,T., Ishiguro,T. and Saito,J.
JOURNAL	Oligonucleotides and method for detection of meca gene of
	methicillin-resistant Staphylococcus aureus
	Patent: EP 1160333-A 27 05-DEC-2001;
	Tosoh Corporation (JP)
FEATURES	Location/Qualifiers
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	/db_xref="taxon:32630"
	/note="Probe"

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Query Match	100.0%; Score 21; DB 6; Length 39;						
Best Local Similarity	100.0%; Pred. No. 9.5e+02;						
Matches 21; Conservative	0; Mismatches 0; Indels 0; Gaps 0;						
OY	1 TTTTCTTTTCTCTATTATG 21						
Db	1 TTTTCTTTTCTCTATTATG 21						
RESULT 4							
LOCUS	E09772	1789 bp	RNA	linear			
DEFINITION	The base sequence of modified meca DNA.						
ACCESSION	E09772						
VERSION	E09772.1	GI:22026401					
KEYWORDS	JP 1995209294-A/2.						
SOURCE	Staphylococcus aureus.						
ORGANISM	Staphylococcus aureus.						
REFERENCE	Bacteria; Firmicutes; Bacillales; Staphylococcus.						
AUTHORS	1 (bases 1 to 1789)						
TITLE	Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.						
JOURNAL	NOVEL 'MECA' PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS						
COMMENT	Patent: JP 1995209294-A 2 11-AUG-1995;						
	KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD						
	OS Staphylococcus aureus						
	PN JP 1995209294-A/2						
	PD 11-AUG-1995						
	PP 10-JAN-1994 JP 1994012226						
	PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI						
	MASAHISA,						
	PI SUGURO KAZUYA						
	PC C01N23/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC						
	C12R1:19)						
	IC (C12P21/02,C12R1:19);						
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	CC topology: Linear;						
	FH Key						
	FH Location/Qualifiers						
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	FT CDS						
	FT						
FEATURES							
source							
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	Location/Qualifiers						
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	/organism='Staphylococcus aureus'						
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Best Local Similarity	100.0%; Pred. No. 4e+02;						
Matches 21; Conservative	0; Mismatches 0; Indels 0; Gaps 0;						
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Db	556 TTTTCTTTTCTCTATTATG 536						
RESULT 5							
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DEFINITION	Sequence 169 from patent US 5994066.						
ACCESSION	AR089410						
VERSION	AR089410.1	GI:10016167					
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 2007)						

AUTHORS Bergeron,M.G., Picard,F.J., Quellerie,M. and Roy,P.H.
TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 5994066-A 169 30-NOV-1999;
FEATURES Location/Qualifiers
SOURCE 1..2007
BASF COUNT 855 a 270 c 341 g 541 t
ORIGIN
Query Match 100.0%; Score 21; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTCTTTTCTCTATTATG 21
DB 955 TTTTCTTTTCTCTATTATG 935
FEATURES
LOCUS AR093610 2007 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 169 from patent US 6001564.
ACCESSION AR093610
VERSION AR093610.1 GI:10020359
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2007)
AUTHORS Bergeron,M.G., Quellerie,M. and Roy,P.H.
TITLE Species specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 6001564-A 169 14-DEC-1999;
FEATURES Location/Qualifiers
SOURCE 1..2007
BASF COUNT 855 a 270 c 341 g 541 t
ORIGIN
Query Match 100.0%; Score 21; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 955 TTTTCTTTTCTCTATTATG 935
RESULT 7
SAPBP/c 2322 bp DNA linear BCT 12-SEP-1993
LOCUS Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible penicillin-binding protein.
ACCESSION Y00688.1 GI:46628
VERSION Y00688
KEYWORDS penicillin-binding protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus
REFERENCE 1 (bases 1 to 2322)
AUTHORS Song,M.D., Machi,M., Dol,M., Ishino,F. and Matsunashi,M.
TITLE Evolution of an inducible penicillin-target protein in methicillin-resistant Staphylococcus aureus by gene fusion
JOURNAL FEBS Lett. 221 (1), 167-171 (1987)
MEDLINE 87304805
PUBMED 3305073
REFERENCE 2 (bases 1 to 2322)
AUTHORS Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,

TITLE Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.
Sequence comparison of mecA genes isolated from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT Data kindly reviewed (13.1.88) by Matsunashi.
FEATURES Location/Qualifiers
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/db_xref="taxon:1280"
1..2013
/note="penicillin-binding protein (AA 1-670)"
/codon_start=1
/transl_table=1
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OKSIYNNKNDYSGSTAIHPOTGELLAVSTFSDVYFPFGMSNEEYKLTEDRKEP
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VNCNIDKQATIESDNIFFAPARVALPLGSKKKEKMKKIGVCHDIIPSDYPIYNAOISNK
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BASE COUNT 940 a 324 c 389 g 669 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTCTTTTCTCTATTATG 21
DB 961 TTTTCTTTTCTCTATTATG 941
RESULT 8
E03736/c 2322 bp DNA linear PAT 29-SEP-1997
LOCUS DNA sequence of PBP2' gene for determination of methicillin resistance.
DEFINITION
ACCESSION E03736
VERSION E03736.1 GI:2171951
KEYWORDS JP 1992169200-A/9.
SOURCE unidentified.
ORGANISM unidentified
REFERENCE 1 (bases 1 to 2322)
AUTHORS Watanabe,Y., Nakamura,E., Teraoka,H., Wada,K., Minamide,N. and Murakami,K.
TITLE Detection of PBP 2' GENE AND JUDGEMENT OF METHICILLIN RESISTANCE
JOURNAL SHIONOGI & CO LTD
COMMENT OS (methicillin resistant)staphylococcus aureus
PN JP 1992169200-A/9
PD 17-JUN-1992
PF 31-OCT-1990 JP 1990296708
PI WATANABE YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI,
PI MINAMIDE MAKIYO, MURAKAMI KAZUHISA
PC C1201/68, C12N15/11;
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers

FT misc-feature 1..2322
FT /note="PBP2' gene for determination of FT
FT methicillin
FT resistance'
FEATURES
source 1..2322
Location/Qualifiers
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/db_xref="taxon:32644"
BASE COUNT 939 a 324 c 390 g 669 t
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Query Match 100.0%; Score 21; DB 6; Length 2322;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCTTTTCTCTATTATG 21
Db 961 TTTCTTTTCTCTATTATG 941
RESULT 9
JMECAPB/C 2454 bp DNA linear BCT 12-SEP-1993
LOCUS SEMECAPB 2454 bp DNA linear BCT 12-SEP-1993
DEFINITION S. epidermidis meca gene for PBP2' (penicillin binding protein 2').
ACCESSION X52592
VERSION X52592.1 GI:46993
KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
penicillin-binding protein 2'.
SOURCE Staphylococcus epidermidis.
ORGANISM Staphylococcus epidermidis.
REFERENCE 1 (bases 1 to 2448)
AUTHORS Bacteria; Firmicutes; Bacillales; Staphylococcus.
TITLE Ryffel, C.
JOURNAL Direct Submission
REFERENCE 2 (bases 1 to 2454)
AUTHORS Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
TITLE Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
Barberis-Maino, L., Kayser, F. H. and Berger-Baechli, B.
Sequence comparison of meca genes from methicillin-resistant
Staphylococcus aureus and Staphylococcus epidermidis
Gene (1990) In press
TITLE 3 (bases 1 to 2454)
AUTHORS Ryffel, C.
JOURNAL Direct Submission
TITLE Submitted (23-JUL-1990) Ryffel C., University of Zuerich, Inst of
Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
4 (bases 1 to 2454)
AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
Barberis-Maino, L., Kayser, F. H. and Berger-Baechli, B.
Sequence comparison of meca genes isolated from
methicillin-resistant Staphylococcus aureus and Staphylococcus
epidermidis
Gene 94 (1), 137-138 (1990)
JOURNAL MEDLINE
PUBMED 91033056
COMMENT See also <X52593-4> and <Y00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.
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/db_xref="taxon:1282"
/clone="WT80/MT79"
80..85
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101..105
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130..134
/note="ribosome binding site"
141..2159
/note="primary transcript"
141..2147
CDS

/note="PBP2' (AA 1 - 668)"
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/db_xref="GI:46994"
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/translation="MKKIKIVPLILIVVVGCHIVPYASNDKFINNTIDAIPKNNKO
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DNEITLADSGGGGELLINVOILSYISALENNGNINAPHLKDTKNKYWKNNIISK
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Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCTTTTCTCTATTATG 21
Db 1095 TTTCTTTTCTCTATTATG 1075
RESULT 10
E09771/C 2455 bp RNA linear PAT 29-SEP-1997
LOCUS E09771
DEFINITION The base sequence of meca DNA.
ACCESSION E09771
VERSION E09771.1 GI:22026400
KEYWORDS JP 1995209294-A/1.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1 (bases 1 to 2455)
AUTHORS Bacteria; Firmicutes; Bacillales; Staphylococcus.
TITLE Kono, M., Hiramatsu, K., Sasazu, M., Noguichi, M. and Suguro, K.
NOVEL MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
Patent: JP 1995209294-A 1 11-AUG-1995;
KONO MECUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/1
PD 11-AUG-1995
PF 10-JAN-1994 JP 1994012226
PI KONO MECUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
MASAHISA,
PI SUGURO KAZUYA
PC G01N33/53, C07K14/31, C12N1/21, C12N15/09, C12P21/02, (C12N1/21, PC
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PC (C12P21/02, C12R1:19);
CC strandedness: Double;
CC topology: Linear;


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FEATURES
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Query Match      100.0%; Score 21; DB 6; Length 2455;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTATG 21
b 1094 TTTTCTTTTCTCTATTATG 1074

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RESULT 11
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LOCUS            S. aureus meca gene for PBP2' (penicillin binding protein 2').
DEFINITION      X52593
ACCESSION       X52593.1 GI:46610
VERSION         meca gene; methicillin resistance; penicillin-binding protein;
KEYWORDS        penicillin-binding protein 2.
SOURCE          Staphylococcus aureus.
ORGANISM        Bacillus: Firmicutes; Bacillales; Staphylococcus.
REFERENCE       1 (bases 1 to 2456)
AUTHORS         Ryffel, C.
TITLE           Direct Submission
JOURNAL         Submitted (05-APR-1990) Ryffel C., University of Zurich, Inst of
REFERENCE       2 (bases 1 to 2456)
AUTHORS         Medical Microbiology, Glorstr 32, CH-8028 Zurich, Switzerland
TITLE           Barbelis-Maino, L., Kayser, F.H. and Berger-Bachl, B.
REFERENCE       Sequence comparison of meca genes isolated from
AUTHORS         methicillin-resistant Staphylococcus aureus and Staphylococcus
TITLE           epidermidis
JOURNAL         Gene 94 (1), 137-138 (1990)
MEDLINE         91033056
PUBMED         2227446
COMMENT         See also <X52592>, <X52594> and <Y00688>.
                  Data kindly reviewed (23-JUL-1990) by C. Ryffel.
FEATURES
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Query Match      100.0%; Score 21; DB 1; Length 2456;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTATG 21
Db 1095 TTTTCTTTTCTCTATTATG 1075

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RESULT 12
AX110445/C       2456 bp  DNA  linear  PAT 30-APR-2001
LOCUS            Sequence 1178 from Patent WO0123604.
DEFINITION      AX110445
ACCESSION       AX110445.1 GI:13926737
VERSION         Staphylococcus aureus subsp. aureus NCTC 8325.
KEYWORDS        Staphylococcus aureus subsp. aureus NCTC 8325.
SOURCE          Staphylococcus aureus subsp. aureus NCTC 8325.
ORGANISM        Bacteria: Firmicutes; Bacillales; Staphylococcus.
REFERENCE       1 (bases 1 to 2456)
AUTHORS         Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
TITLE           Picard, F.J. and Roy, P.H.
JOURNAL         Highly conserved genes and their use to generate probes and primers
REFERENCE       for detection of microorganisms
AUTHORS         Patent: WO 0123604-A 1178 05-APR-2001;
TITLE           Infectio Diagnostic (I.D.I.) INC. (CA)
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BASE COUNT      1001 a 344 c 396 g 715 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTATG 21
Db 1095 TTTTCTTTTCTCTATTATG 1075

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RESULT 13
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LOCUS            S. sciuri meca gene & ORF's 450, 145 & 179.
DEFINITION      Y09223
ACCESSION       Y09223.1 GI:2073520
VERSION         meca gene.
KEYWORDS        Staphylococcus sciuri.
SOURCE          Staphylococcus sciuri.
ORGANISM        Bacteria: Firmicutes; Bacillales; Staphylococcus.
REFERENCE       1 (bases 1 to 5068)
AUTHORS         Wu, S., Piscitelli, C., de Lencastre, H. and Tomasz, A.
TITLE           Tracking the evolutionary origin of the methicillin resistance
JOURNAL         gene: cloning and sequencing of a homologue of meca from a
REFERENCE       methicillin-susceptible strain of Staphylococcus sciuri
AUTHORS         Michrb. Drug Res. 2, 435-441 (1996)
TITLE           2 (bases 1 to 5068)
JOURNAL         Direct Submission
AUTHORS
TITLE

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JOURNAL Submitted (05-NOV-1996) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York, NY 10021, USA
REFERENCE 3 (bases 1 to 5068)
AUTHORS Wu, S.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York, NY 10021, USA
COMMENT On May 8, 1997 this sequence version replaced gi:1769448.
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complement(1413..1418)
/note="ORF450"
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4532..45068
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BASE COUNT 1887 a 837 c 833 g 1511 t
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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;
Oy 1 TTTCTTTTCTATTATG 21
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RESULT 14
SSK8MECA 5596 bp DNA linear BCT 16-JAN-1998
LOCUS S_sciuri meca gene, strain K8 (ATCC700063).
DEFINITION
ACCESSION Y13096
VERSION Y13096.1 GI:2791919
KEYWORDS meca gene; mecI gene; mecR1 gene; NTORF101; NTORF78; ORF142.
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 5596)
Wu, S., de Lencastre, H. and Tomasz, A.
Genetic organization of the meca region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus sciuri
J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE 94101461
PUBMED 9440511
REFERENCE
2 (bases 1 to 5596)
Wu, S.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences X53818, X54660, L14020, X52593, Y09223.
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COMMENT	Related sequences J14020. X53593. Y09223.			
JOURNAL	Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York NY 10021, USA			
AUTHORS	Wu, S.			
REFERENCE	2 (bases 1 to 6368)			
PUBMED	9440511			
LOCUS	SSK3MECA2			
DEFINITION	S. sciuri meca2 gene, strain K3 (MM2).			
ACCESSION	Y13095			
VERSION	Y13095.1			
KEYWORDS	GI:2791912			
SOURCE	C10RF261 gene; meca2 gene; mecI gene; mecR1 gene; N10RF101; ORF142.			
ORGANISM	Staphylococcus sciuri			
REFERENCE	Bacteria: Firmicutes: Bacillales: Staphylococcus.			
AUTHORS	1 (bases 1 to 6368)			
TITLE	Wu, S., de Lencastre, H. and Tomasz, A.			
JOURNAL	Genetic organization of the meca region in methicillin-susceptible and methicillin-resistant strains of Staphylococcus sciuri			
PUBMED	J. Bacteriol. 180 (2), 236-242 (1998)			
LOCUS	9440511			
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ACCESSION	Wu, S.			
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KEYWORDS	Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York NY 10021, USA			
ORGANISM	Related sequences J14020. X53593. Y09223.			
REFERENCE	Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York NY 10021, USA			
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REFERENCE	Bacteria: Firmicutes: Bacillales: Staphylococcus.			
AUTHORS	1 (bases 1 to 6368)			
TITLE	Wu, S., de Lencastre, H. and Tomasz, A.			
JOURNAL	Genetic organization of the meca region in methicillin-susceptible and methicillin-resistant strains of Staphylococcus sciuri			
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DEFINITION	2 (bases 1 to 6368)			
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ORGANISM	Staphylococcus sciuri			
REFERENCE	Bacteria: Firmicutes: Bacillales: Staphylococcus.			
AUTHORS	1 (bases 1 to 6368)			
TITLE	Wu, S., de Lencastre, H. and Tomasz, A.			
JOURNAL	Genetic organization of the meca region in methicillin-susceptible and methicillin-resistant strains of Staphylococcus sciuri			
PUBMED	J. Bacteriol. 180 (2), 236-242 (1998)			
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DEFINITION	2 (bases 1 to 6368)			
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REFERENCE	Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York NY 10021, USA			
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PUBMED	J. Bacteriol. 180 (2), 236-242 (1998)			
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DEFINITION	2 (bases 1 to 6368)			
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VERSION	Direct Submission			
KEYWORDS	Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York NY 10021, USA			
ORGANISM	Related sequences J14020. X53593. Y09223.			
REFERENCE	Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller University, 1230 York Avenue, New York NY 10021, USA			
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ORGANISM	Staphylococcus sciuri			
REFERENCE	Bacteria: Firmicutes: Bacillales: Staphylococcus.			
AUTHORS	1 (bases 1 to 6368)			
TITLE	Wu, S., de Lencastre, H. and Tomasz, A.			
JOURNAL	Genetic organization of the meca region in methicillin-susceptible and methicillin-resistant strains of Staphylococcus sciuri			
PUBMED				

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gene	complement(1636. .1640) /gene="mec1"
RBS	complement(1636. .1640) /gene="mec1"
RBS	complement(3392. .3398) /gene="mecr1"
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gene	3424. .3429 /gene="mecr1"
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BASE COUNT    2230 a          998 c          884 g         2256 t  
ORIGIN  
  
Query Match    100.0%; Score 21; DB 1; Length 6368;  
Best Local Similarity 100.0%; Pid. No. 3e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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               |||||  
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Search completed: December 10, 2002, 20:16:49  
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 : Search time 303.542 Seconds
(without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579A-19
Perfect score: 14
Sequence: 1 gaagagtgcttac 14

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenBank:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
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36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	14	100.0	14 6 AX306858	AX306858 Sequence
2	14	100.0	14 6 AX306860	AX306860 Sequence
3	14	100.0	467 6 AA4526	AA4526 Sequence 2
4	14	100.0	720 6 HSA336539	AJ336539 Homo sapi
5	14	100.0	1789 6 E09772	E09772 The base se
6	14	100.0	2007 6 AR089410	AR089410 Sequence
7	14	100.0	2007 6 AR093610	AR093610 Sequence
8	14	100.0	2322 6 SAPBP	Y00688 Staphylococ
9	14	100.0	2322 6 E03736	E03736 DNA sequenc
10	14	100.0	2454 6 SEMECAPB	X52592 S. epidermi
11	14	100.0	2455 6 E09771	E09771 The base se
12	14	100.0	2456 6 SAMECAPB	X52593 S. aureus m
13	14	100.0	2456 6 AX110445	AX110445 Sequence
14	14	100.0	5596 1 SSK8MECA	Y13096 S. sciuri me
15	14	100.0	6368 1 SSK3MECA2	Y14051 Staphylococ
16	14	100.0	9047 1 SAMECARIT	AE000716 Aquillex a
17	14	100.0	14567 1 AE000716	AE000716 Staphyloc
18	14	100.0	21777 1 AB063173	AB063173 Staphyloc
19	14	100.0	26090 1 AB063172	AB063172 Staphyloc
20	14	100.0	39332 1 AB033763	AB033763 Staphyloc
21	14	100.0	42689 8 SPC330	AI031603 S. pombe c
22	14	100.0	58237 1 D86934	D86934 Staphylococ
23	14	100.0	62311 9 AL157716	AL157716 Human DNA
24	14	100.0	63672 2 AC114608	AC114608 Mus muscu
25	14	100.0	68256 1 AB037671	AB037671 Staphyloc
26	14	100.0	80301 2 AC097768	AC097768 Rattus no
27	14	100.0	81650 8 NCB9815	AL451014 Neurospor
28	14	100.0	95155 9 AC078950	AC078950 Homo sapi
29	14	100.0	110000 9 AF440620_2	Continuation (3 of
30	14	100.0	126427 9 AL161424	AL161424 Human DNA
31	14	100.0	133387 2 AP004061	AP004061 Oryza sat
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33	14	100.0	147599 2 AC126088	AC126088 Rattus no
34	14	100.0	155803 9 AC090799	AC090799 Homo sapi
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37	14	100.0	172612 2 AC110523	AC110523 Mus muscu
38	14	100.0	175485 2 AC111539	AC111539 Rattus no
39	14	100.0	183502 2 AC117454	AC117454 Homo sapi
40	14	100.0	184245 2 AC097819	AC097819 Rattus no
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ALIGNMENTS

RESULT 1
AX306858
LOCUS AX306858 14 bp DNA
DEFINITION Sequence 17 from Patent EP1160333.
ACCESSION AX306858
VERSION AX306858.1 GI:11894680
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.

REFERENCE
AUTHORS Taya, T., Ishiguro, T. and Saito, J.
TITLE Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
JOURNAL Patent: EP 1160333-A 17 05-DEC-2001

FEATURES Tosoh Corporation (JP)
Location/Qualifiers
1. 14
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide capable of binding specifically to
meca gene or RNA derived from said gene"

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14
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Db 1 GAAGTGTGCTTAC 14

RESULT 2
LOCUS AX306860 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 19 from Patent EPL160333.
ACCESSION AX306860
VERSION AX306860.1 GI:17894682
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Taya, T., Ishiguro, T. and Saito, J.
TITLE Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
JOURNAL Patent: EP 1160333-A 19 05-DEC-2001;
Tosoh Corporation (JP)
LOCATION/Qualifiers
1. 14
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/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 3 a 2 c 5 g 4 t
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OY 1 GAAGTGTGCTTAC 14
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1 GAAGTGTGCTTAC 14

RESULT 3
LOCUS A44526 467 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 2 from Patent WO9513395.
ACCESSION A44526
VERSION A44526.1 GI:2299344
KEYWORDS
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1
AUTHORS Springer, W. and Endermann, R.
TITLE SPECIFIC GENE PROBES AND METHODS FOR QUANTITATIVE DETECTION OF
METHICILLIN-RESISTANT STAPHYLOCOCCI
JOURNAL Patent: WO 9513395-A 2 18-MAY-1995;
Bayer AG (DE)
Other publication DE 4338119 950511.
COMMENT 1. 467
Location/Qualifiers
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 70 GAAGTGTGCTTAC 57

RESULT 4
LOCUS HSA336539 720 bp DNA linear PRI 18-JUL-2002
DEFINITION HSA336539
HSA336539 Homo sapiens genomic sequence surrounding NOL1 site, clone
NRL-PF5C.
ACCESSION AJ336539
VERSION AJ336539.1 GI:15880957
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1
AUTHORS Kutsenko, A.S., Glatzullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,
Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,
Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I.,
Kisselev, L.L., Masserman, M., Mahlestedt, C. and Zbarovsky, E.R.
TITLE NOL1 flanking sequences: a tool for gene discovery and verification
of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 2231767
PUBMED 12136098
REFERENCE 2 (bases 1 to 720)
AUTHORS Zbarovsky, E.R.
TITLE Direct Substitution
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorigenology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
LOCATION/Qualifiers
1. 720
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NRL-PF5C"

BASE COUNT 113 a 203 c 211 g 193 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 457 GAAGTGTGCTTAC 470

RESULT 5
LOCUS E09772 1789 bp RNA linear PAT 29-SEP-1997
DEFINITION The base sequence of modified meca DNA.
ACCESSION E09772
VERSION E09772.1 GI:22026401
KEYWORDS JP 1995209294-A/2.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1
AUTHORS Kono, M., Hiramatsu, K., Sasazu, M., Noguchi, M. and Suguro, K.
TITLE NOVEL 'MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL Patent: JP 1995209294-A 2 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD

```
COMMENT OS Staphylococcus aureus
          PN JP 1995209294-A/2
          PD 11-AUG-1995
          PI 10-JAN-1994 JP 1994012226
          PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
          MASAHISA,
          PI SUGURO KAZUYA
          PC G01N33/53.C07K14/31.C12M1/21.C12M15/09.C12P21/02.(C12M1/21, PC
          C12R1.19)
          CC (C12P21/02.C12R1.19);
          CC strandedness: Double;
          CC topology: Linear;
          FI Key location/Qualifiers
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          FT 1..1608 /organism='Staphylococcus aureus' FT CDS
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          1..1789
          /organism='Staphylococcus aureus'
          /db_xref='taxon:1280'
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Host Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14
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Db 695 GAAGTGTGCTTAC 682

RESULT 6
AR089410/c AR089410 2007 bp DNA Linear PAT 07-SEP-2000
LOCUS AR089410
DEFINITION Sequence 169 from patent US 5994066.
ACCESSION AR089410
VERSION AR089410.1 GI:10016167
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2007)
          Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.
          Species-specific and universal DNA probes and amplification primers
          to rapidly detect and identify common bacterial pathogens and
          associated antibiotic resistance genes from clinical specimens for
          routine diagnosis in microbiology laboratories
          Patent: US 5994066-A 169 30-NOV-1999;
          location/Qualifiers
          source 1..2007
          /organism='unknown'
          BASE COUNT 855 a 270 c 341 g 541 t
          ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14
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Db 1094 GAAGTGTGCTTAC 1081

RESULT 7
AR093610/c AR093610 2007 bp DNA Linear PAT 08-SEP-2000
LOCUS AR093610
DEFINITION Sequence 169 from patent US 6001564.
ACCESSION AR093610
VERSION AR093610.1 GI:10020359
KEYWORDS
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2007)
          Bergeron,M.G., Ouellette,M. and Roy,P.H.
          Species specific and universal DNA probes and amplification primers
          to rapidly detect and identify common bacterial pathogens and
          associated antibiotic resistance genes from clinical specimens for
          routine diagnosis in microbiology laboratories
          Patent: US 6001564-A 169 14-DEC-1999;
          location/Qualifiers
          source 1..2007
          /organism='unknown'
          BASE COUNT 855 a 270 c 341 g 541 t
          ORIGIN

Query Match 100.0%; Score 14; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGTGTGCTTAC 14
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Db 1094 GAAGTGTGCTTAC 1081

RESULT 8
SAPHP 2322 bp DNA Linear ACT 12-SEP-1993
LOCUS SAPHP/c
DEFINITION Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible
          penicillin-binding protein.
          Y00688
          Y00688.1 GI:46628
          penicillin-binding protein.
          KEYWORDS Staphylococcus aureus.
          SOURCE Staphylococcus aureus
          ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
          REFERENCE 1 (bases 1 to 2322)
          AUTHORS Song,M.D., Machl,M., Dol,M., Ishino,F. and Matsushashi,M.
          Evolution of an inducible penicillin-target protein in
          methicillin-resistant Staphylococcus aureus by gene fusion
          PNAS Lett. 221 (1), 167-171 (1987)
          JOURNAL MEDLINE
          PUBMED 87304805
          REFERENCE 2 (bases 1 to 2322)
          AUTHORS Kyffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E.,
          Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.
          Sequence comparison of mecA genes isolated from
          methicillin-resistant Staphylococcus aureus and Staphylococcus
          epidermidis
          Gene 94 (1), 137-138 (1990)
          JOURNAL MEDLINE
          PUBMED 91033056
          COMMENT 2227446
          FEATURES Data kindly reviewed (13.1.88) by Matsushashi.
          source location/Qualifiers
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          /note='penicillin-binding protein (AA 1-670)'
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          KMDVEYLSDFAKKHLTNTFTESRNVPIGKATSHLAGVGPINSEELKQKDYKQKDA
          VIGKKGLEKLYDKKLOHEDGVRVTVIVVDNSNTIARTLIEKKKDKDIOILTIDAKV
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Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGCTGCTTAC 14
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Db 1234 GAAGCTGCTTAC 1221

RESULT 11
E09771/c 2455 bp RNA linear PAT 29-SEP-1997
'OCUS The base sequence of meca DNA.
'INITIATION E09771
'CESSION E09771.1 GI:22026400
KEYWORDS JP 1995209294-A/1.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
REFERENCE 1 (bases 1 to 2455)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS Kono, M., Hiramatsu, K., Sasazu, M., Noguchi, M. and Suguro, K.
TITLE NOVEL "MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL Patent: JP 1995209294-A 1 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/1
PD 11-AUG-1995
PP 10-JAN-1994 JP 1994012226
PT KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI MASAHISA,
PI SUGURO KAZUYA
PC G01N33/53.C07K14/31.C12N1/21.C12N15/09.C12P21/02.(C12N1/21, PC C12R1.19),
PC (C12P21/02, C12R1.19);
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
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FT 134..2146 /organism="Staphylococcus aureus" FT CDS
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source Location/Qualifiers
1..2455
/organism="Staphylococcus aureus"
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BASE COUNT 997 a 344 c 401 g 713 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGCTGCTTAC 14
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Db 1233 GAAGCTGCTTAC 1220

RESULT 12
SAMECAPB/c 2456 bp DNA linear BCT 12-SEP-1993
LOCUS SAMECAPB
DEFINITION S. aureus meca gene for PBP2' (penicillin binding protein 2').
ACCESSION X52593
VERSION X52593.1 GI:46610

KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;
penicillin-binding protein 2.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 2456)
AUTHORS Ryffel, C.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
2 (bases 1 to 2456)
REFERENCE Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P.F.,
Barberis-Maino, L., Kayser, F.H. and Berger-Bachi, B.
AUTHORS Sequence comparison of meca genes isolated from
methicillin-resistant Staphylococcus aureus and Staphylococcus
epidermidis
JOURNAL Gene 94 (1), 137-138 (1990)
MEDLINE 91033056
PUBMED 2227446
COMMENT See also <X52592>, <X52594> and <Y00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.

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source Location/Qualifiers
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/strain="NCIC8325, isolate=B8270"
/db_xref="taxon:1280"
/clone_lib="EMBL-3"
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101..105
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130..134
/note="ribosome binding site"
141..2153
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141..2147
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ELANTGTHMRLLGIIVPKNVSKKDYKAKAIKELISIEDYINNKWKIGYKMPSEHFTVK
KMEYLSDFAKKPHLTTNETESRNPYLEKATSHLGVGPIINSEELKQKEYGKDDA
VIGKGLKLYDKKLOHEDGQRYVTIVDQNSNTIAHLLEKKKKDKDLOLTIDAKYOK
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NKFOITTSFGSTOKIITAMIGLNNKTLIDIKTSYKIDGCKMOKDKSMGYNVTRIEYVN
GNTDLQALLESSDNIFPARVALELGSKEKFKGKKRGVGEDIPSDPFPYNAOISNVL
DNELDLADSGYGGGELLINPVOLISYLSALENNGNINAPHLIKDTNKNVAKRNIIISKE
NINLNDGQQVYVNTKHEIDYRSYANLIGKSGTAEKMKKQSGSGROIGWFTSYDDKN
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BASE COUNT 1001 a 344 c 396 g 715 t
ORIGIN

Query Match 100.0%; Score 14; DB 1; Length 2456;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGCTGCTTAC 14
|||||
Db 1234 GAAGCTGCTTAC 1221

RESULT 13
AX110445/c 2456 bp DNA linear PAT 30-APR-2001
LOCUS AX110445
DEFINITION Sequence 1178 from Patent WO0123604.
ACCESSION AX110445
VERSION AX110445.1 GI:13926737
KEYWORDS


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Query Match      100.0%; Score 14; DB 1; Length 5596;
Best Local Similarity 100.0%; Pred. No. 5,1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 GAAGTGCTTAC 14
Db      3806 GAAGCTGCTTAC 3793

RESULT 15
SSK3MECA2/c      6368 bp      DNA      linear      BCT 16-JAN-1998
DEFINITION      S.sciuri meca2 gene, strain K3 (MM2).
ACCESSION      Y13095
VERSION      Y13095.1 GI:2791912
KEYWORDS      CTORF261 gene; meca2 gene; mecI gene; mecR1 gene; NTOF101; ORF142.
SOURCE      Staphylococcus sciuri.
ORGANISM      Staphylococcus sciuri
REFERENCE      Bacteria; Firmicutes; Bacillales; Staphylococcus.
AUTHORS      Wu, S., de Lencastre, H. and Tomasz, A.
TITLE      Genetic organization of the meca region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus sciuri
JOURNAL      J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE      98101461
PubMed      9440511
REFERENCE      2 (bases 1 to 6368)
AUTHORS      Wu, S.
TITLE      Direct Submission
JOURNAL      Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
COMMENT      Related sequences L14020, X52593, Y09223.
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HETBGSISLAKKI KETTPVAVVNEANISALYERNFNHNLISNNILALS IHKGIGACL
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY 1 GAAGGTGCTTAC 14
DB 4578 GAAGGTGCTTAC 4565

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 Job time : 307.667 secs

Thu Dec 12 09:59:04 2002

us-09-865-579a-19.rni

Gencore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 ; Search time 19.0838 Seconds
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	2007	2 US-08-743-637B-169	Sequence 169, App
2	14	100.0	2007	3 US-08-526-840B-169	Sequence 1710, App
3	14	100.0	2028	4 US-09-134-001C-1770	Sequence 336, App
4	13	92.9	1758	4 US-09-620-412C-336	Sequence 1, Appl
5	13	92.9	2068	1 US-08-309-341-1	Sequence 1, Appl
6	13	92.9	2068	1 US-08-608-267-1	Sequence 1, Appl
7	13	92.9	2068	1 US-08-608-452-1	Sequence 1, Appl
8	13	92.9	2068	1 US-08-608-224-1	Sequence 1, Appl
9	13	92.9	2068	1 US-08-967-149-1	Sequence 1, Appl
10	13	92.9	5265	4 US-09-556-877-174	Sequence 174, App
11	13	92.9	5265	4 US-09-620-412C-174	Sequence 104, App
12	13	92.9	6735	4 US-08-961-527-104	Sequence 357, App
13	12.4	88.6	807	4 US-08-961-527-357	Patent No. 5223425
14	12.4	88.6	863	6 5223425-1	Patent No. 5223425
15	12.4	88.6	1029	1 US-07-809-457A-15	Sequence 15, Appl
16	12.4	88.6	1029	1 US-08-553-943-15	Sequence 15, Appl
17	12.4	88.6	1029	5 PCT-US91-09437-15	Sequence 2, Appl
18	12.4	88.6	1393	1 US-08-052-205-2	Sequence 2, Appl
19	12.4	88.6	1393	1 US-08-595-974-2	Sequence 9, Appl
20	12.4	88.6	1416	4 US-09-330-611-9	Sequence 68, Appl
21	12.4	88.6	1451	4 US-08-031-143B-68	Sequence 3, Appl
22	12.4	88.6	1470	1 US-08-052-205-3	Sequence 3, Appl
23	12.4	88.6	1470	1 US-08-595-974-3	Sequence 1, Appl
24	12.4	88.6	2070	1 US-08-394-326-1	Sequence 1, Appl
25	12.4	88.6	2070	3 US-09-082-306-1	Sequence 19, Appl
26	12.4	88.6	3987	1 US-07-688-352C-19	Sequence 19, Appl
27	12.4	88.6	3987	1 US-07-688-352C-19	Sequence 19, Appl

28	12.4	88.6	3987	2 US-08-474-379C-19	Sequence 19, Appl
29	12.4	88.6	3987	3 US-09-146-249A-19	Sequence 19, Appl
30	12.4	88.6	3987	5 US-08-206-188B-19	Sequence 19, Appl
31	12.4	88.6	3987	5 PCT-US91-02714-19	Sequence 182, App
32	12.4	88.6	4550	4 US-09-338-907-182	Sequence 4, Appl
33	12.4	88.6	4550	4 US-09-218-207-182	Sequence 4, Appl
34	12.4	88.6	5816	4 US-09-220-641-4	Sequence 49, Appl
35	12.4	88.6	7898	4 US-08-984-709A-49	Sequence 65, Appl
36	12.4	88.6	11831	4 US-08-961-527-65	Sequence 66, App
37	12.4	88.6	50000	4 US-09-146-053-3	Sequence 769, App
38	12.4	85.7	330	4 US-09-134-001C-686	Sequence 1, Appl
39	12	85.7	877	4 US-09-605-785-769	Sequence 3, Appl
40	12	85.7	2026	2 US-08-559-492-1	Sequence 11, Appl
41	12	85.7	2368	4 US-09-343-011B-3	Sequence 12, Appl
42	12	85.7	3488	4 US-08-930-285-12	Sequence 1, Appl
43	12	85.7	3544	4 US-08-697-826A-11	Sequence 1, Appl
44	12	85.7	4315	2 US-08-781-802-1	Sequence 1, Appl
45	12	85.7	4315	4 US-08-694-078-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-743-637B-169/C
Sequence 169, Application US/08743637B

Patent No. 5994066

GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.

APPLICANT: PICARD, Francois J.

APPLICANT: QUELETTE, Marc

APPLICANT: ROY, Paul H.

TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATEDTITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

TITLE OF INVENTION: 273

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS: QUARLES & BRADY

STREET: 411 EAST WISCONSIN AVENUE

CITY: MILWAUKEE

STATE: WISCONSIN

COUNTRY: USA

ZIP: 53202-4497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patconlin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/743,637B

CLASSIFICATION: 435

FILING DATE: 04-NOV-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/526,840

FILING DATE: 11-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: BAKER, Jean C. 35,433

REGISTRATION NUMBER: 850586,90012

REFERENCE/DOCKET NUMBER: 850586,90012

TELEPHONE: (414) 277-5000

TELEFAX: (414) 277-5591

INFORMATION FOR SEQ ID NO: 169:

SEQUENCE CHARACTERISTICS:

LENGTH: 2007 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-743-637B-169

Query Match

100.0% Score 14: DB 2: Length 2007:

Best Local Similarity 100.0%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C/ 1 GAAGGTGCTTAC 14
Db 1094 GAAGGTGCTTAC 1081

RESULT 2
US-08-526-840B-169/C
Sequence 169, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: APPLICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
S-08-526-840B-169

Query Match 100.0%; Score 14; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1094 GAAGGTGCTTAC 1081

RESULT 3
S-09-134-001C-1710/C
Sequence 1710, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1710
LENGTH: 2028
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
FEATURE:
NAME/KEY: unsure
LOCATION: (52)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

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Best Local Similarity 100.0%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1115 GAAGGTGCTTAC 1102

RESULT 4
US-09-620-412C-336/C
Sequence 336, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121,469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 336
LENGTH: 1758
TYPE: DNA
ORGANISM: Chlamydia trachomatis
US-09-620-412C-336

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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGGTGCTTAC 13
Db 1451 GAAGGTGCTTAC 1439

RESULT 5
US-08-309-341-1/C
Sequence 1, Application US/08309341
Patent No. 5594119
GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Thompson, Sheryl Ann
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5594119g NO. 5594119g disk of No. 5594119th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,341
FILING DATE: 16-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4247, 000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger
FEATURE:
NAME/KEY: intron
LOCATION: 572..632
FEATURE:
NAME/KEY: CDS
LOCATION: join (571..633)
US-08-309-341-1

Query Match          92.9%; Score 13; DB 1; Length 2068;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      2 AAGCTGCTTAC 14
DB      583 AAGCTGCTTAC 571

RESULT 6
US-08-608-267-1/c
Sequence 1, Application US/08608267
Patent No. 5688663
GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Thompson, Sheryl Ann
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5688663disk of No. 5688663ln America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,267
FILING DATE: 28-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,341
FILING DATE: 20-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4247, 000-US
TELECOMMUNICATION INFORMATION:
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TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger
FEATURE:
NAME/KEY: intron
LOCATION: 572..632
FEATURE:
NAME/KEY: CDS
LOCATION: join (571..633)
US-08-608-267-1
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Query Match          92.9%; Score 13; DB 1; Length 2068;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      2 AAGCTGCTTAC 14
DB      583 AAGCTGCTTAC 571
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RESULT 7
US-08-608-452-1/c
Sequence 1, Application US/08608452
Patent No. 5693510
GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Thompson, Sheryl Ann
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5693510disk of No. 5693510ln America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,452
FILING DATE: 28-FEB-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,341
FILING DATE: 20-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4247, 000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Aspergillus niger
FEATURE:
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NAME/KEY: inton
LOCATION: 572..632
FEATURE:
NAME/KEY: CDS
LOCATION: join (571..633)
US-08-608-452-1

Query Match 92.9%; Score 13; DB 1; Length 2068;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 583 AAGCTGCTTAC 571

RESULT 8
US-08-608-224-1/c

Sequence 1, Application US/08608224
Patent No. 5705376
GENERAL INFORMATION:

APPLICANT: Yaver, Debbie Sue
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57053760 No. 5705376disk of No. 5705376th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,224
FILING DATE: 28-FEB-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/309,341
FILING DATE: 20-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.

REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4247,000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2068 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

ORIGINAL SOURCE:

ORGANISM: Aspergillus niger

FEATURE:

NAME/KEY: intron

LOCATION: 572..632

FEATURE:

NAME/KEY: CDS

LOCATION: join (571..633)
US-08-608-224-1

Query Match 92.9%; Score 13; DB 1; Length 2068;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 AAGCTGCTTAC 14

|||||
DB 583 AAGCTGCTTAC 571

RESULT 9
US-08-967-149-1/c

Sequence 1, Application US/08967149
Patent No. 5939305
GENERAL INFORMATION:

APPLICANT: Yaver, Debbie Sue
TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59393050 No. 5939305disk of No. 5939305th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,149
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/608,452
FILING DATE: 28-FEB-1996
APPLICATION NUMBER: US 08/309,341
FILING DATE: 20-SEP-1994

ATTORNEY/AGENT INFORMATION:
NAME: Lowney, Karen A.

REGISTRATION NUMBER: 31,274

REFERENCE/DOCKET NUMBER: 4247,000-US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2068 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

ORIGINAL SOURCE:

ORGANISM: Aspergillus niger

FEATURE:

NAME/KEY: intron

LOCATION: 572..632

FEATURE:

NAME/KEY: CDS

LOCATION: join (571..633)
US-08-967-149-1

Query Match 92.9%; Score 13; DB 2; Length 2068;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AAGTGTCTTAC 14
|||||
DB 583 AAGTGTCTTAC 571

RESULT 10
US-09-556-877-174/c
Sequence 174, Application US/09556877
Patent No. 6432916
GENERAL INFORMATION:

APPLICANT: Probst, Peter
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yassir
APPLICANT: Fling, Steve
APPLICANT: Maisonneuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556.877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 174
LENGTH: 5265
TYPE: DNA
ORGANISM: Chlamydia
US-09-556-877-174

Query Match 92.9%; Score 13; DB 4; Length 5265;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTA 13
Db 2003 GAAGGTGCTTA 1991

RESULT 11
US-09-620-412C-174/C
Sequence 174, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620.412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 174
LENGTH: 5265
TYPE: DNA
ORGANISM: Chlamydia
US-09-620-412C-174

Query Match 92.9%; Score 13; DB 4; Length 5265;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTA 13
Db 2003 GAAGGTGCTTA 1991

RESULT 12
US-08-961-527-104/C
Sequence 104, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961.527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 6735 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-104

Query Match 92.9%; Score 13; DB 4; Length 6735;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGCTTAC 14
Db 5983 AAGGTGCTTAC 5971

RESULT 13
US-08-961-527-357
Sequence 357, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961.527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 357:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-961-527-357

Query Match 88.6%; Score 12.4; DB 4; Length 807;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
||||| |||||
DB 499 GAAGTTTGTCTTAC 512

RESULT 14

5223425-1
; Patent No. 5223425
; APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,
; BARRY M.; WHITE, TYLER R.
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
; ID ACTIVITY
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/277,963
; FILING DATE: 30-NOV-1988
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 34,203
; FILING DATE: 02-APR-1987
; SEQ ID NO: 1:
; LENGTH: 863
5223425-1

Query Match 88.6%; Score 12.4; DB 6; Length 863;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGTGTGCTTAC 14
||||| |||||
DB 668 GAAGTGTGCTTAC 681

RESULT 15
5223425-9
; Patent No. 5223425
; APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,
; BARRY M.; WHITE, TYLER R.
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
; ID ACTIVITY
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/277,963
; FILING DATE: 30-NOV-1988
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 34,203
; FILING DATE: 02-APR-1987
; SEQ ID NO: 9:
; LENGTH: 863
5223425-9

Query Match 88.6%; Score 12.4; DB 6; Length 863;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGTGTGCTTAC 14
||||| |||||
DB 673 GAAGTGTGCTTAC 686

Search completed: December 10, 2002, 22:54:21
Job time : 21.2088 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 : Search time 18.1453 Seconds
(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-19

Perfect score: 14
Sequence: 1 gaaggtgtgtcttac 14

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_MA:*

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- 2: /cgn2_6/ptodata/2/pubna/PTCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubna/US07_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubna/PCRTS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubna/US08_NEW_PUB.seq:*
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- 12: /cgn2_6/ptodata/2/pubna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	14	10	US-09-865-579A-17
2	14	100.0	14	10	US-09-865-579A-19
3	14	100.0	2007	10	US-09-452-599-159
4	13	92.9	1758	10	US-09-841-132-421
5	13	92.9	5253	10	US-09-841-132-421
6	13	92.9	5253	10	US-09-841-132-556
7	13	92.9	5253	10	US-09-841-132-174
8	12.4	88.6	233	10	US-09-983-965-5426
9	12.4	88.6	399	10	US-09-815-242-9114
10	12.4	88.6	399	10	US-09-815-242-9114
11	12.4	88.6	408	10	US-09-783-590-3620
12	12.4	88.6	418	10	US-09-960-352-12566
13	12.4	88.6	459	10	US-09-864-761-1021
14	12.4	88.6	500	10	US-09-783-590-3621
15	12.4	88.6	759	10	US-09-974-300-2230
16	12.4	88.6	995	12	US-10-021-509-4
17	12.4	88.6	995	12	US-10-021-509-12
18	12.4	88.6	1173	9	US-09-938-842A-1515
19	12.4	88.6	1187	10	US-09-801-574-47

C	20	12.4	88.6	1323	10	US-09-815-242-9609	Sequence 9609, Ap
C	21	12.4	88.6	1416	9	US-09-891-641-70	Sequence 70, Appl
C	22	12.4	88.6	1416	9	US-09-847-010-9	Sequence 9, Appl1
C	23	12.4	88.6	1451	10	US-09-880-107-1595	Sequence 1595, Ap
C	24	12.4	88.6	1451	10	US-09-822-849A-159	Sequence 159, Ap
C	25	12.4	88.6	1836	10	US-09-864-761-16939	Sequence 16939, A
C	26	12.4	88.6	1836	9	US-09-938-842A-2286	Sequence 2286, Ap
C	27	12.4	88.6	4087	10	US-09-901-419-1	Sequence 1, Appl1
C	28	12.4	88.6	4550	9	US-09-853-526-182	Sequence 182, App
C	29	12.4	88.6	4550	10	US-09-901-484A-182	Sequence 182, App
C	30	12.4	88.6	4683	9	US-09-070-927A-193	Sequence 193, App
C	31	12.4	88.6	7642	10	US-09-938-842A-43	Sequence 43, Appl
C	32	12.4	88.6	10024	10	US-09-880-107-2430	Sequence 2430, Ap
C	33	12.4	88.6	32134	10	US-09-764-847-1057	Sequence 1057, Ap
C	34	12.4	88.6	32134	10	US-09-764-847-1535	Sequence 1535, Ap
C	35	12.4	88.6	32187	10	US-09-764-847-1530	Sequence 1530, Ap
C	36	12.4	88.6	32193	10	US-09-764-847-1549	Sequence 1549, Ap
C	37	12.4	88.6	167343	10	US-09-962-436-281	Sequence 281, App
C	38	12.4	88.6	167343	10	US-09-964-824A-273	Sequence 273, App
C	39	12.4	88.6	465237	10	US-09-933-267A-1	Sequence 1, Appl1
C	40	12	85.7	103	10	US-09-783-590-9007	Sequence 9007, Ap
C	41	12	85.7	149	10	US-09-969-273-548	Sequence 548, App
C	42	12	85.7	160	10	US-09-864-761-32198	Sequence 32198, A
C	43	12	85.7	160	10	US-09-864-761-32240	Sequence 32240, A
C	44	12	85.7	165	10	US-09-815-242-2248	Sequence 2248, Ap
C	45	12	85.7	165	10	US-09-815-242-2261	Sequence 2261, Ap

ALIGNMENTS

RESULT 1
US-09-865-579A-17
Sequence 17, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865, 579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to meca gene
; OTHER INFORMATION: or RNA derived from said gene
US-09-865-579A-17
Query Match 100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAGTGTCCTTAC 14
DB 1 GAAGTGTCCTTAC 14
RESULT 2
US-09-865-579A-19
Sequence 19, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:

APPLICANT: Taya, Toshiki
APPLICANT: Ishiguro, Takahiko
TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
FILE REFERENCE: 9558-003-27
CURRENT APPLICATION NUMBER: US/09/865,579A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: JP 2000-163149
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-179394
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
S-09-865-579A-19

Query Match 100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGCTTAC 14
Db 1 GAAGCTGCTTAC 14

RESULT 3
US-09-452-599-169/c
Sequence 169, Application US/09452599
Patent No. US20020055101A1
GENERAL INFORMATION:
APPLICANT: Bergeron, Michel G.
APPLICANT: Roy, Paul H.
TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
FILE REFERENCE: 1287.31
CURRENT APPLICATION NUMBER: US/09/452,599
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 08/526,840
PRIOR FILING DATE: 1995-09-11
PRIOR APPLICATION NUMBER: 08/304,732
PRIOR FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 177
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 169
LENGTH: 2007
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match 100.0%; Score 14; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGCTTAC 14
Db 1094 GAAGCTGCTTAC 1081

RESULT 4
US-09-841-132-336/c
Sequence 336, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 336
LENGTH: 1758
TYPE: DNA
ORGANISM: Chlamydia trachomatis
US-09-841-132-336

Query Match 92.9%; Score 13; DB 10; Length 1758;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGCTTA 13
Db 1451 GAAGCTGCTTA 1439

RESULT 5
US-09-841-132-421/c
Sequence 421, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 421
LENGTH: 5253
TYPE: DNA
ORGANISM: Chlamydia trachomatis serovar D
US-09-841-132-421

Query Match 92.9%; Score 13; DB 10; Length 5253;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGCTGCTTA 13
Db 1994 GAAGCTGCTTA 1982

RESULT 6
US-09-841-132-556/c
Sequence 556, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 556
LENGTH: 5253
TYPE: DNA
ORGANISM: C. Trachomatis D serovar

US-09-841-132-556

Query Match
Best Local Similarity 92.9%; Score 13; DB 10; Length 5253;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGGTGCTTAC 13
|||||
Db 1994 GAAGGTGCTTAC 1982

RESULT 7

US-09-841-132-174/C
; Sequence 174, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 174
; LENGTH: 5265
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-841-132-174

Query Match
Best Local Similarity 92.9%; Score 13; DB 10; Length 5265;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAGGTGCTTAC 13
|||||
Db 2003 GAAGGTGCTTAC 1991

RESULT 8

US-09-983-965-5426
; Sequence 5426, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengding
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 5426
; LENGTH: 233
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 44-LIB34-067-01-EI-C8
US-09-983-965-5426

Query Match
Best Local Similarity 88.6%; Score 12.4; DB 10; Length 233;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GAAGGTGCTTAC 14

Db 118 GAAGGTGCTTAC 131
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RESULT 9

US-09-815-242-9114
; Sequence 9114, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9114
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(399)
US-09-815-242-9114

Query Match
Best Local Similarity 88.6%; Score 12.4; DB 10; Length 399;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GAAGGTGCTTAC 14
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Db 328 GAAGGTGCTTAC 341

RESULT 10

US-09-815-242-9472
; Sequence 9472, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242

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: CURRENT FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9472
: LENGTH: 399
: TYPE: DNA
: ORGANISM: Streptococcus pneumoniae
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(399)
: US-09-815-242-9472
Query Match      88.6%: Score 12.4; DB 10; Length 399;
Best Local Similarity 92.9%: Pred. No. 2.1e+02;
Matches 13: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY      1 GAAGCTGTCCTTAC 14
        ||||| |||||
Db       328 GAAGTTGCTTAC 341
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RESULT 11
: US-09-783-590-3620
: Sequence 3620, Application US/09783590
: Patent No. US20020110850A1
: GENERAL INFORMATION:
: APPLICANT: Dillon, Patrick J.
: APPLICANT: Haseltine, William A.
: APPLICANT: Li, Haodong
: APPLICANT: Rosen, Craig A.
: APPLICANT: Ruben, Steven M.
: TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
: FILE REFERENCE: PO-16,2C1
: CURRENT FILING DATE: 2000-02-15
: PRIOR APPLICATION NUMBER: 08/420,856
: PRIOR FILING DATE: 1995-04-12
: PRIOR APPLICATION NUMBER: 08/346,731
: PRIOR FILING DATE: 1994-11-21
: NUMBER OF SEQ ID NOS: 12485
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3620
: LENGTH: 408
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (73)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (320)
: OTHER INFORMATION: n equals a,t,g, or c
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: LOCATION: (340)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (352)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
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: LOCATION: (356)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (399)
: OTHER INFORMATION: n equals a,t,g, or c
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: NAME/KEY: misc feature
: LOCATION: (406)
: OTHER INFORMATION: n equals a,t,g, or c
: US-09-783-590-3620
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Best Local Similarity 92.9%: Pred. No. 2.1e+02;
Matches 13: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY      1 GAAGCTGTCCTTAC 14
        ||||| |||||
Db       299 GAAGCTGCTTAC 312
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RESULT 12
: US-09-960-352-12566/C
: Sequence 12566, Application US/09960352
: Patent No. US20020137139A1
: GENERAL INFORMATION:
: APPLICANT: Warren, Wesley C.
: APPLICANT: Tao, Ningbing
: APPLICANT: Byatt, John C.
: APPLICANT: Mathaiagan, Nagappan
: TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION ANI
: FILE REFERENCE: 16511.006/37-21(10298)C
: CURRENT FILING DATE: 2001-09-24
: NUMBER OF SEQ ID NOS: 15112
: SEQ ID NO 12566
: LENGTH: 418
: TYPE: DNA
: ORGANISM: Bos laurus
: OTHER INFORMATION: Clone ID: 54-LIB188-016-Q1-E1-F10
: US-09-960-352-12566
Query Match      88.6%: Score 12.4; DB 10; Length 418;
Best Local Similarity 92.9%: Pred. No. 2.1e+02;
Matches 13: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY      1 GAAGCTGTCCTTAC 14
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Db       66 GAAGGTGCTGAC 53
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RESULT 13
: US-09-864-761-102
: Sequence 102, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
: FILE REFERENCE: Aeomica-X-1
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
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? PRIOR APPLICATION NUMBER: GB 24263.6
? PRIOR FILING DATE: 2000-10-04
? PRIOR APPLICATION NUMBER: US 60/236,359
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: PCT/US01/00666
? PRIOR FILING DATE: 2001-01-30
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? PRIOR APPLICATION NUMBER: PCT/US01/00664
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? PRIOR APPLICATION NUMBER: PCT/US01/00669
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00665
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00668
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00663
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? PRIOR APPLICATION NUMBER: PCT/US01/00662
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00661
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00670
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 09/608,408
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: US 09/774,203
? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 49117
? SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
? SEQ ID NO 102
? LENGTH: 459
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AC007281.3
? OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
? OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.68
? OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.69
? OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.1
? OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.83
? OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
? OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
? US-09-864-761-102
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Best Local Similarity 92.9%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 GAAGGTGCTTAC 14
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DB      143 GAAGCTTCTTAC 156
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RESULT 14

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US-09-783-590-3621
? Sequence 3621, Application US/09783590
? Patent No. US2002010850A1
? GENERAL INFORMATION:
? APPLICANT: Dillon, Patrick J.
? APPLICANT: Haseltine, William A.
? APPLICANT: Li, Haodong
? APPLICANT: Rosen, Craig A.
? APPLICANT: Ruben, Steven M.
? TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
? FILE REFERENCE: PO-16.2c1
? CURRENT APPLICATION NUMBER: US/09/783,590
? PRIOR APPLICATION NUMBER: 08/420,856
? PRIOR FILING DATE: 1995-04-12
? PRIOR APPLICATION NUMBER: 08/346,731
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? PRIOR FILING DATE: 1994-11-21
? NUMBER OF SEQ ID NOS: 12485
? SOFTWARE: Patentl Ver. 2.0
? SEQ ID NO 3621
? LENGTH: 500
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (73)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
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? NAME/KEY: misc feature
? LOCATION: (240)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (246)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (275)
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? NAME/KEY: misc feature
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? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
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? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
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? NAME/KEY: misc feature
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? OTHER INFORMATION: n equals a,t,g, or c
? US-09-783-590-3621
Query Match      88.6%; Score 12.4; DB 10; length 500;
Best Local Similarity 92.9%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 GAAGGTGTCTTAC 14
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Db 301 GAAGGTGTCTTAC 314

RESULT 15

US-09-974-300-2230
; Sequence 2230, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2230
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2230

Query Match 88.6%; Score 12.4; DB 10; Length 759;
Best Local Similarity 92.9%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GAAGGTGTCTTAC 14
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Db 550 GAAGGTGTCTTAC 563

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Job time : 20.1453 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 : Search time 36.2905 Seconds
(without alignments)
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Title: US-09-865-579A-18

Perfect score: 28
Sequence: 1 aattgggtacagatgatacttcgtt 28

Scoring table:
IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_MA:*

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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	10	US-09-865-579A-18 Sequence 18, Appl
2	28	100.0	2007	10	US-09-452-599-169 Sequence 169, App
3	18	64.3	232	10	US-09-880-107-262 Sequence 262, App
4	18	64.3	277	10	US-09-920-300A-1187 Sequence 1187, App
5	18	64.3	277	12	US-10-033-528-1187 Sequence 1187, App
6	18	64.3	1079	10	US-09-834-975-802 Sequence 802, App
7	17.8	63.6	2000	9	US-09-938-842A-2769 Sequence 2769, App
8	17.6	62.9	4329	10	US-09-815-242-3949 Sequence 3949, App
9	17.6	62.9	4356	10	US-09-815-242-6637 Sequence 6637, App
10	17.6	62.9	21252	10	US-09-070-927A-94 Sequence 94, Appl
11	17.4	62.1	1233	10	US-09-974-300-2472 Sequence 2472, Appl
12	17.4	62.1	1318	10	US-09-826-508-27 Sequence 27, Appl
13	17.4	62.1	1987	10	US-09-917-800A-1338 Sequence 1338, App
14	17.4	62.1	12445	10	US-09-070-927A-242 Sequence 242, App
15	17.4	62.1	15745	10	US-09-764-877-3236 Sequence 3236, App
16	17.2	61.4	339	10	US-09-867-701-6331 Sequence 6331, App
17	17.2	61.4	421	10	US-09-867-701-6415 Sequence 6415, App
18	17	60.7	213	10	US-09-878-574-14790 Sequence 14790, A
19	17	60.7	293	10	US-09-738-973-534 Sequence 534, App

20	17	60.7	3612	10	US-09-880-107-2353 Sequence 2353, App
21	17	60.7	6147	9	US-09-938-842A-2441 Sequence 2441, App
22	17	60.7	7923	10	US-09-864-864-297 Sequence 297, App
23	16.8	60.0	164	10	US-09-878-574-11991 Sequence 11991, A
24	16.8	60.0	264	10	US-09-815-343-89 Sequence 89, Appl
25	16.8	60.0	376	10	US-09-783-590-11404 Sequence 11404, A
26	16.8	60.0	393	9	US-10-046-935-2142 Sequence 2142, App
27	16.8	60.0	393	9	US-09-878-178-2142 Sequence 2142, App
28	16.8	60.0	476	10	US-09-864-761-10674 Sequence 10674, A
29	16.8	60.0	1116	9	US-09-931-457A-12 Sequence 12, Appl
30	16.8	60.0	8395	10	US-09-070-927A-217 Sequence 217, App
31	16.8	60.0	15613	10	US-09-878-574-11991 Sequence 3525, App
32	16.8	60.0	31208	10	US-09-852-067-3 Sequence 3, Appl
33	16.8	60.0	198285	10	US-09-880-107-3814 Sequence 3814, App
34	16.6	59.3	394	10	US-09-878-574-2552 Sequence 2552, App
35	16.6	59.3	580	10	US-09-864-761-12786 Sequence 12786, A
36	16.4	58.6	180	10	US-09-923-876-1440 Sequence 1440, A
37	16.4	58.6	296	10	US-09-960-352-11565 Sequence 11565, A
38	16.4	58.6	339	10	US-09-974-300-5204 Sequence 5204, App
39	16.4	58.6	422	10	US-09-864-761-3746 Sequence 3746, App
40	16.4	58.6	430	10	US-09-864-761-1508 Sequence 1508, App
41	16.4	58.6	462	10	US-09-867-701-4231 Sequence 4231, App
42	16.4	58.6	552	10	US-09-974-300-3811 Sequence 3811, App
43	16.4	58.6	3700	10	US-09-917-800A-1539 Sequence 1539, App
44	16.2	57.9	93	10	US-09-864-761-26662 Sequence 26662, A
45	16.2	57.9	360	10	US-09-974-300-8286 Sequence 8286, App

ALIGNMENTS

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RESULT 1
US-09-865-579A-18
: Sequence 18, Application US/09865579A
: Patent No. US20020098492A1
: GENERAL INFORMATION:
: APPLICANT: Taya, Toshiki
: APPLICANT: Ishiguro, Takahiko
: TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
: FILE REFERENCE: 9558-003-27
: CURRENT APPLICATION NUMBER: US/09/865,579A
: PRIOR FILING DATE: 2001-05-29
: PRIOR APPLICATION NUMBER: JP 2000-163149
: PRIOR FILING DATE: 2000-05-29
: PRIOR APPLICATION NUMBER: JP 2000-179394
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 18
: LENGTH: 28
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Primer
US-09-865-579A-18

Query Match      100.0%; Score 28; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 A A A T T G G T A C A G A T G A T C C T T C G T T 28
Db      1 A A A T T G G T A C A G A T G A T C C T T C G T T 28

RESULT 2
US-09-452-599-169
: Sequence 169, Application US/09452599
: Patent No. US20020055101A1
: GENERAL INFORMATION:
: APPLICANT: Bergeron, Michel G.
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; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: To Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; US-09-452-599-169

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Query Match          100.0%; Score 28; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AATTGGCTACAGATGATGATCTTGGTT 28
Db 608 AATTGGCTACAGATGATGATCTTGGTT 635

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RESULT 3
US-09-880-107-262
; Sequence 262, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 262
; LENGTH: 232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA129390
; US-09-880-107-262

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Query Match          64.3%; Score 18; DB 10; Length 232;
Best Local Similarity 80.8%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 3 ATTGGTACAGATGATGATCTTGGTT 28
Db 172 ATTGGTACAGATGATGATCTTGGTT 197

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RESULT 4
US-09-920-300A-1187
; Sequence 1187, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy

```

```

; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1187
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-920-300A-1187

```

```

Query Match          64.3%; Score 18; DB 10; Length 277;
Best Local Similarity 80.8%; Pred. No. 15;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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```

QY 3 ATTGGTACAGATGATGATCTTGGTT 28
Db 89 ATTGGTACAGATGATGATCTTGGTT 114

```

```

RESULT 5
US-10-033-528-1187
; Sequence 1187, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: F-astSeq for Windows Version 4.0
; SEQ ID NO 1187
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-033-528-1187

```

```

Query Match          64.3%; Score 18; DB 12; Length 277;
Best Local Similarity 80.8%; Pred. No. 15;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 3 ATTGGTACAGATGATGATCTTGGTT 28
Db 89 ATTGGTACAGATGATGATCTTGGTT 114

```

```

RESULT 6
US-09-834-975-802/C
; Sequence 802, Application US/09834975
; Patent No. US20020110815A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Brown, Jeffrey
; APPLICANT: Bolt, Andrew
; APPLICANT: Van Hulle, Christophe
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-0168
; CURRENT APPLICATION NUMBER: US/09/834,975
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046

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```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 802
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1079)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-975-802

Query Match
Best Local Similarity 64.3%; Score 18; DB 10; Length 1079;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 ATTGGGTACAGATGATACCTTCGTT 28
    ||| ||||| ||||| ||| ||
Db 781 ATTGCTACAGATGATACCTTCGTT 756

RESULT 7
US-09-938-842A-2769/C
; Sequence 2769, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2769
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2769

Query Match
Best Local Similarity 63.6%; Score 17.8; DB 9; Length 2000;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GTACAGATGATACCTTCGTT 28
    || ||||| ||||| |||||
Db 1603 GTCCAGATGATACCTTCGTT 1583

RESULT 8
US-09-815-242-3949
; Sequence 3949, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
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; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3949
; LENGTH: 4329
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-3949

Query Match
Best Local Similarity 62.9%; Score 17.6; DB 10; Length 4329;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 TTGGTACAGATGATACCTTCGT 27
    || ||||| ||||| |||||
Db 894 TAGTGTACAGATGATACCTTCAT 917

RESULT 9
US-09-815-242-6637
; Sequence 6637, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6637
; LENGTH: 4356
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4356)
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; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1338
; LENGTH: 1987
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 D38381
; US-09-917-800A-1338

Query Match      62.1%; Score 17.4; DB 10; Length 1987;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 21: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 AATTGGGTACAGATGATACCTTCGTT 28
DB      1166 AATTGGGTACATCTTAGACTTCATT 1140

RESULT 14
US-09-070-927A-242
; Sequence 242, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
;              Patrick J. Dillon
;              Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,555
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
```

```

; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12445 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
; US-09-070-927A-242

Query Match      62.1%; Score 17.4; DB 10; Length 12445;
Best Local Similarity 77.8%; Pred. No. 65;
Matches 21: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 AATTGGGTACAGATGATACCTTCGTT 28
DB      11938 AATGGGACACGACAGATATATTTCGTT 11964

RESULT 15
US-09-764-877-3236
; Sequence 3236, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3236
; LENGTH: 15745
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-877-3236

Query Match      62.1%; Score 17.4; DB 10; Length 15745;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 21: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 AATTGGGTACAGATGATACCTTCGTT 28
DB      4132 AATTGGACACATGCAAAATTAATTTCGTT 4158
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Search completed: December 11, 2002, 06:03:06
Job time : 45.2905 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 ; Search time 38.1676 Seconds
(Without alignments)
224,980 Million cell updates/sec

Title: US-09-865-579A-18

Perfect score: 28
Sequence: 1 aaatgggacaaagatgacatcgtt 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Capext 1.0

Searched: 44362 seqs, 15338381 residues

Jcal number of hits satisfying chosen parameters: 682724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	2007	2 US-08-743-637B-169	Sequence 169, App
2	28	100.0	2007	3 US-08-526-840B-169	Sequence 169, App
3	28	100.0	2028	4 US-09-134-001C-1710	Sequence 1710, App
4	17.4	62.1	1318	3 US-09-183-253-3	Sequence 3, App1
5	17.4	62.1	4249	4 US-09-071-035-403	Sequence 403, App
6	17.4	62.1	4359	4 US-09-071-035-401	Sequence 401, App
7	17.4	62.1	84495	4 US-09-797-906-3	Sequence 3, App1
8	16.8	60.0	1379	4 US-09-499-505-6	Sequence 6, App1
9	16.8	60.0	1379	4 US-09-626-410-6	Sequence 6, App1
10	16.8	60.0	1379	4 US-09-116-188-6	Sequence 6, App1
11	16.8	60.0	1379	4 US-09-626-047-6	Sequence 6, App1
12	16.8	60.0	1379	4 US-09-626-343-6	Sequence 6, App1
13	16.8	60.0	1379	4 US-09-354-922-7	Sequence 7, App1
14	16.8	60.0	2539	1 US-07-885-970A-28	Sequence 28, App1
15	16.8	60.0	2539	1 US-08-298-687A-28	Sequence 28, App1
16	16.8	60.0	2539	1 US-08-298-829-28	Sequence 28, App1
17	16.8	60.0	28171	4 US-08-961-527-22	Sequence 22, App1
18	16.8	58.6	585	3 US-08-882-501-28	Sequence 28, App1
19	16.4	58.6	51259	3 US-08-781-891-209	Sequence 209, App
20	16.2	57.9	2268	4 US-09-351-414-1	Sequence 1, App1
21	16.2	57.9	4854	4 US-08-961-527-178	Sequence 178, App
22	16.2	57.9	112132	4 US-09-741-150-3	Sequence 3, App1
23	16	57.1	3054	4 US-08-961-527-183	Sequence 183, App
24	16	57.1	14654	4 US-08-961-527-106	Sequence 106, App
25	16	57.1	4411529	4 US-09-103-840A-1	Sequence 1, App1
26	15.8	56.4	542	4 US-09-173-300-27	Sequence 27, App1
27	15.8	56.4	731	4 US-09-328-111-438	Sequence 438, App

C 28	15.8	56.4	1343	4	US-09-499-505-5	Sequence 5, App1
C 29	15.8	56.4	1343	4	US-09-626-410-5	Sequence 5, App1
C 30	15.8	56.4	1343	4	US-09-116-188-5	Sequence 5, App1
C 31	15.8	56.4	1343	4	US-09-626-047-5	Sequence 5, App1
C 32	15.8	56.4	1343	4	US-09-626-343-5	Sequence 5, App1
C 33	15.8	56.4	1343	4	US-09-354-922-6	Sequence 6, App1
C 34	15.8	56.4	1380	4	US-09-499-505-4	Sequence 4, App1
C 35	15.8	56.4	1380	4	US-09-626-410-4	Sequence 4, App1
C 36	15.8	56.4	1380	4	US-09-116-188-4	Sequence 4, App1
C 37	15.8	56.4	1380	4	US-09-626-047-4	Sequence 4, App1
C 38	15.8	56.4	1380	4	US-09-626-343-4	Sequence 4, App1
C 39	15.8	56.4	1380	4	US-09-354-922-5	Sequence 5, App1
C 40	15.8	56.4	1382	4	US-09-499-505-2	Sequence 2, App1
C 41	15.8	56.4	1382	4	US-09-626-410-2	Sequence 2, App1
C 42	15.8	56.4	1382	4	US-09-116-188-2	Sequence 2, App1
C 43	15.8	56.4	1382	4	US-09-626-047-2	Sequence 2, App1
C 44	15.8	56.4	1382	4	US-09-626-343-2	Sequence 2, App1
C 45	15.8	56.4	1382	4	US-09-354-922-3	Sequence 3, App1

ALIGNMENTS

```
RESULT 1
US-08-743-637B-169
: Sequence 169, Application US/08743637B
: Patent No. 5994066
:
: GENERAL INFORMATION:
: APPLICANT: BERGERON, Michel G.
: APPLICANT: PICARD, Francois J.
: APPLICANT: ROY, Paul H.
: APPLICANT: OUELLETTE, Marc
: TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
: TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
: TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
: TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
: NUMBER OF SEQUENCES: 273
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OUALES & BRADY
: STREET: 411 EAST WISCONSIN AVENUE
: CITY: MILWAUKEE
: STATE: WISCONSIN
: COUNTRY: USA
: ZIP: 53202-4497
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/743,637B
: FILING DATE: 04-NOV-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/526,840
: FILING DATE: 11-SEP-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: BAKER, Jean C.
: REGISTRATION NUMBER: 35,433
: REFERENCE/DOCKET NUMBER: 850586,90012
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (414) 277-5000
: TELEFAX: (414) 277-5591
: INFORMATION FOR SEQ ID NO: 169:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2007 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-743-637B-169
:
: Query Match 100.0%; Score 28; DB 2; Length 2007;
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Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGGGTACAGATGATACCTTGCTT 28
|||||
Db 608 AATGGGTACAGATGATACCTTGCTT 635

RESULT 2

US-08-526-840B-169
Sequence 169, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: OVARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGGGTACAGATGATACCTTGCTT 28
|||||
Db 608 AATGGGTACAGATGATACCTTGCTT 635

RESULT 3

US-09-134-001C-1710
Sequence 1710, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucelte-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1710
LENGTH: 2028
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
FEATURE:
NAME/KEY: unsure
LOCATION: (52)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 28; DB 4; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATGGGTACAGATGATACCTTGCTT 28
|||||
Db 630 AATGGGTACAGATGATACCTTGCTT 657

RESULT 4

US-09-183-253-3/C
Sequence 3, Application US/09183253
Patent No. 6043054
GENERAL INFORMATION:
APPLICANT: VAMTER, LISA
APPLICANT: STAMERS, MELANIE
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,253
FILING DATE: 30-OCT-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9817907.0
FILING DATE: 17-AUG-1998
APPLICATION NUMBER: 60/075,306
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70395
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-183-253-3


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US-09-499-505-6/C
: Sequence 6, Application US/09499505
: Patent No. 6251674
: GENERAL INFORMATION:
: APPLICANT: DEL CARDAYRE, STEPHEN
: APPLICANT: TOBIN, MATTHEW
: APPLICANT: STEMMER, WILLEM P.C.
: APPLICANT: NESS, JON E.
: APPLICANT: MINSHULL, JEREMY
: APPLICANT: PATTEN, PHILLIP
: APPLICANT: SUBRAMANIA, VENKITSWARAN
: APPLICANT: CASTLE, LINDA
: APPLICANT: KREBER, CLAUS M.
: APPLICANT: BASS, STEVE
: TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
: TITLE OF INVENTION: SEQUENCE RECOMBINATION
: FILE REFERENCE: 02-020720US
: CURRENT APPLICATION NUMBER: US/09/499,505
: CURRENT FILING DATE: 2000-02-07
: PRIOR APPLICATION NUMBER: 09/116,188
: PRIOR FILING DATE: 1998-07-15
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 1379
: TYPE: DNA
: ORGANISM: Escherichia coli
US-09-499-505-6

Query Match          60.0%; Score 16.8; DB 4; Length 1379;
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 GTACAAGATGATACCTTCGT 27
      ||| ||| ||| ||| ||| ||| |||
DB      1061 GTACAAGTGTGATACCTTCGT 1042

RESULT 9
US-09-626-410-6/C
: Sequence 6, Application US/09626410
: Patent No. 6287862
: GENERAL INFORMATION:
: APPLICANT: DEL CARDAYRE, STEPHEN
: APPLICANT: TOBIN, MATTHEW
: APPLICANT: STEMMER, WILLEM P.C.
: APPLICANT: NESS, JON E.
: APPLICANT: MINSHULL, JEREMY
: APPLICANT: PATTEN, PHILLIP
: APPLICANT: SUBRAMANIA, VENKITSWARAN
: APPLICANT: CASTLE, LINDA
: APPLICANT: KREBER, CLAUS M.
: APPLICANT: BASS, STEVE
: TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
: TITLE OF INVENTION: SEQUENCE RECOMBINATION
: FILE REFERENCE: 02-020720US
: CURRENT APPLICATION NUMBER: US/09/626,410
: CURRENT FILING DATE: 2000-07-26
: PRIOR APPLICATION NUMBER: 09/116,188
: PRIOR FILING DATE: 07-15-1998
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 1379
: TYPE: DNA
: ORGANISM: Escherichia coli
US-09-626-410-6

Query Match          60.0%; Score 16.8; DB 4; Length 1379;
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y      8 GTACAAGATGATACCTTCGT 27

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      ||| ||||| ||||||||| |||
Db    1061 GTGAAGTTGATACCTTCTGT 1042

RESULT 10
US-09-116-188-6/c
; Sequence 6, Application US/09116188
; Patent No. 6326204
; GENERAL INFORMATION:
; APPLICANT: DEL CARDAYRE, STEPHEN
; APPLICANT: TOBIN, MATTHEW
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: NESS, JON E.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: PATTEN, PHILLIP
; APPLICANT: SUBRAMANIA, VENKITSAMARAN
; APPLICANT: CASTLE, LINDA
; APPLICANT: KREBER, CLAUD M.
; APPLICANT: BASS, STEVE
; TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
FILE REFERENCE: 02-02072005
CURRENT FILING DATE: 2000-07-26
PRIORITY APPLICATION NUMBER: 09/116,188
PRIOR FILING DATE: 07-15-1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 1379
TYPE: DNA
ORGANISM: Escherichia coli
US-09-626-047-6

Query Match          60.0%; Score 16.8; DB 4; Length 1379;
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

QY      8 GTACAAGATGATACCTGTCT 27
      ||| ||||| ||||||||| |||
Db    1061 GTGAAGTTGATACCTTCTGT 1042

RESULT 11
US-09-626-047-6/c
; Sequence 6, Application US/09626047
; Patent No. 6335198
; GENERAL INFORMATION:
; APPLICANT: DEL CARDAYRE, STEPHEN
; APPLICANT: TOBIN, MATTHEW
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: NESS, JON E.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: PATTEN, PHILLIP
; APPLICANT: SUBRAMANIA, VENKITSAMARAN
; APPLICANT: CASTLE, LINDA
; APPLICANT: KREBER, CLAUD M.
; APPLICANT: BASS, STEVE
; TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
FILE REFERENCE: 02-02072005
CURRENT FILING DATE: 2000-07-26
PRIORITY APPLICATION NUMBER: 09/116,188
PRIOR FILING DATE: 07-15-1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 1379
TYPE: DNA
ORGANISM: Escherichia coli
US-09-116-188-6

Query Match          60.0%; Score 16.8; DB 4; Length 1379;
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

```

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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 GTACAGATGATACCTTCGT 27
   ||| ||| ||| ||| ||| ||| |||
Db 1061 GTAGAGTGTGATACCTTCGT 1042

RESULT 12
US-09-626-343-6/C
; Sequence 6, Application US/09626343
; Patent No. 6352859
; GENERAL INFORMATION:
; APPLICANT: DEL CARDAYRE, STEPHEN
; APPLICANT: TOBIN, MATTHEW
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: NESS, JON E.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: PATRIN, PHILIP
; APPLICANT: SUBRAMANIA, VENKATESWARAN
; APPLICANT: CASTLE, LINDA
; APPLICANT: KREBER, CLAUD M.
; APPLICANT: BASS, STEVE
; TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
; FILE REFERENCE: 02-02072705
; CURRENT APPLICATION NUMBER: US/09/626,343
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 09/116,188
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-626-343-6

Query Match 60.0%; Score 16.8; DB 4; Length 1379;
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 GTACAGATGATACCTTCGT 27
   ||| ||| ||| ||| ||| ||| |||
Db 1061 GTAGAGTGTGATACCTTCGT 1042

RESULT 13
US-09-354-922-7/C
; Sequence 7, Application US/09354922
; Patent No. 6379964
; GENERAL INFORMATION:
; APPLICANT: DEL CARDAYRE, STEPHEN
; APPLICANT: TOBIN, MATTHEW
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: NESS, JON E.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: PATRIN, PHILIP
; APPLICANT: SUBRAMANIAN, VENKATESWARAN
; APPLICANT: CASTLE, LINDA A.
; APPLICANT: KREBER, CLAUD M.
; APPLICANT: BASS, STEVE
; APPLICANT: ZHANG, YING-XIN
; APPLICANT: COX, TONY
; APPLICANT: HUISMAN, GJALT
; APPLICANT: YUAN, LING
; APPLICANT: AFFHOLTER, JOSEPH A.
; TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
; FILE REFERENCE: 02-02073005
; CURRENT APPLICATION NUMBER: US/09/354,922
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentln Ver. 2.0
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; SEQ ID NO 7
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-354-922-7

Query Match 60.0%; Score 16.8; DB 4; Length 1379;
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 GTACAGATGATACCTTCGT 27
   ||| ||| ||| ||| ||| ||| |||
Db 1061 GTAGAGTGTGATACCTTCGT 1042

RESULT 14
US-07-885-970A-28/C
; Sequence 28, Application US/07885970A
; Patent No. 5495070
; GENERAL INFORMATION:
; APPLICANT: John, Malliyakal E.
; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
; STREET: P.O. Box 2113, First Wisconsin Plaza
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/885,970A
; FILING DATE: 19920518
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/617,239
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 283-2478
; TELEFAX: (608) 251-5139
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2539 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Gossypium barbadense
; STRAIN: Sea Island
; IMMEDIATE SOURCE:
; LIBRARY: EMBL-SI
; CLONING: S1B8
US-07-885-970A-28

Query Match 60.0%; Score 16.8; DB 1; Length 2539;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 AAATGGTACAGATGATACCTTCGT 28
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rb 910 AAGTAGTAAATATGCTACTTAGTT 883

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RESULT 15
; US-08-298-687A-28/c
; Sequence 28: Application US/08298687A
; Patent No. 5521078
; GENERAL INFORMATION:
; APPLICANT: John, Malyakal E.
; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
; TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
; STREET: P.O. Box 2113, First Wisconsin Plaza
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53701
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,687A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/617,239
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 283-2478
; TELEFAX: (608) 251-5139
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2539 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
; ORIGINAL SOURCE:
; ORGANISM: Gossypium barbadense
; STRAIN: Sea Island
; IMMEDIATE SOURCE:
; LIBRARY: EMBL-SI
; CLONE: STB8
;
; US-08-298-687A-28

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Query Match 60.0%; Score 16.8; DB 1; Length 2539;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 AAATTGGTACAGATGATACCTTCGTT 28
Db 910 AAGTAGTAAATATGCTACTTAGTT 883

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Search completed: December 10, 2002, 22:54:19
Job time : 58.2926 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 : Search time 38.1676 Seconds
(without alignments)
224.980 Million cell updates/sec

Title: US-09-865-579a-22

Perfect score: 28

Sequence: 1 aagaagaaagatgcgaagatattcaa 28

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/lna/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/lna/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/lna/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	2007	2	US-08-743-637B-169
2	28	100.0	2007	3	US-08-526-840B-169
3	28	100.0	2028	4	US-09-134-001C-1710
4	20	71.4	29	3	US-09-109-957-4
5	20	71.4	29	3	US-09-109-957-5
6	20	71.4	2775	1	US-08-149-096A-1
7	20	71.4	2830	4	US-09-221-017B-730
8	19.8	70.7	1747	1	US-07-808-455A-2
9	18.8	67.1	1863	2	US-08-455-073A-3
10	18.6	66.4	2415	4	US-09-134-001C-2381
11	18.6	66.4	6156	4	US-08-891-640-1
12	18.6	66.4	6156	4	US-09-723-535-3
13	18.4	65.7	273	2	US-08-737-298-1
14	18.4	65.7	345	4	US-09-328-111-506
15	18.4	65.7	1240	1	US-08-248-466B-6
16	18.4	65.7	1430	4	US-09-357-251-17
17	18.4	65.7	1510	1	US-08-248-466B-3
18	18.4	65.7	1532	1	US-08-248-466B-11
19	18.4	65.7	1972	1	US-08-463-048-1
20	18.4	65.7	1972	1	US-08-463-229-1
21	18.4	65.7	1972	2	US-08-302-891-1
22	18.4	65.7	2040	1	US-08-599-252-103
23	18.4	65.7	2040	5	PCT-US96-06352-103
24	18.4	65.7	2040	5	PCT-US96-06583-103
25	18.4	65.7	2558	4	US-08-936-165A-214
26	18.4	65.7	2892	2	US-08-874-186-44
27	18.4	65.7	4157	2	US-08-871-266B-1

C 28	18.4	65.7	4157	2	US-08-819-458A-1	Sequence 1, Appl
C 29	18.4	65.7	4157	2	US-09-018-864A-1	Sequence 1, Appl
C 30	18.4	65.7	4157	3	US-08-871-267B-1	Sequence 1, Appl
C 31	18.4	65.7	4157	3	US-09-618-419-1	Sequence 1, Appl
C 32	18.4	65.7	14855	2	US-08-687-080-59	Sequence 59, Appl
C 33	18	64.3	39	3	US-08-975-902-47	Sequence 47, Appl
C 34	18	64.3	39	3	US-09-251-565-47	Sequence 47, Appl
C 35	18	64.3	1879	4	US-09-601-091-1	Sequence 1, Appl
C 36	18	64.3	2024	4	US-09-601-091-3	Sequence 3, Appl
C 37	18	64.3	2024	4	US-09-398-395A-51	Sequence 51, Appl
C 38	17.8	63.6	24	1	US-07-808-455A-6	Sequence 6, Appl
C 39	17.8	63.6	1907	4	US-09-443-184-40	Sequence 40, Appl
C 40	17.6	62.9	774	4	US-09-134-001C-2190	Sequence 2190, Ap
C 41	17.6	62.9	2626	4	US-09-632-538C-35	Sequence 35, Appl
C 42	17.6	62.9	22481	4	US-08-367-841A-43	Sequence 43, Appl
C 43	17.6	62.9	22481	5	PCT-US95-07201-43	Sequence 43, Appl
C 44	17.6	62.9	22484	4	US-09-875-223-2	Sequence 2, Appl
C 45	17.4	62.1	57	1	US-08-044-506B-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-743-637B-169
Sequence 169, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
NUMBER OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
TITLE OF INVENTION: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: OVARLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743, 637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526, 840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586, 90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0%; Score 28; DB 2; Length 2007;

Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCAAGATATTCA 28
Db 948 AAAGAAAAAGATGCAAGATATTCA 975

RESULT 2

US-08-526-840B-169
Sequence 169, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: OUELLETTE & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526, 840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850,86,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5500
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:

SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCAAGATATTCA 28
Db 948 AAAGAAAAAGATGCAAGATATTCA 975

RESULT 3

US-09-134-001C-1710
Sequence 1710, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucellette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1710

LENGTH: 2028
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
FEATURE:
NAME/KEY: unsure
LOCATION: (52)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.

US-09-134-001C-1710

Query Match 100.0%; Score 28; DB 4; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCAAGATATTCA 28
Db 969 AAAGAAAAAGATGCAAGATATTCA 996

RESULT 4

US-09-109-957-4
Sequence 4, Application US/09109957
Patent No. 6136533
GENERAL INFORMATION:
APPLICANT: Bekkaoui, Faouzi
APPLICANT: Modrusan, Zora D.
APPLICANT: Pische, Isabelle A.
APPLICANT: Duck, Peter D.
APPLICANT: Cloney, Lynn P.
APPLICANT: Wong, Alfred C.K.
TITLE OF INVENTION: ADDITIVES FOR USE IN CYCLING PROBE REACTIONS
FILE REFERENCE: 480094,419
CURRENT APPLICATION NUMBER: US/09/109,957
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Product of

US-09-109-957-4

Query Match 71.4%; Score 20; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCAAG 20
Db 10 AAAGAAAAAGATGCAAG 29

RESULT 5

US-09-109-957-5/C
Sequence 5, Application US/09109957
Patent No. 6136533
GENERAL INFORMATION:
APPLICANT: Bekkaoui, Faouzi
APPLICANT: Modrusan, Zora D.
APPLICANT: Pische, Isabelle A.
APPLICANT: Duck, Peter D.
APPLICANT: Cloney, Lynn P.
APPLICANT: Wong, Alfred C.K.


```
Sequence 2, Application US/07808455A
Patent No. 5405745
GENERAL INFORMATION:
APPLICANT: Gorman, Jessica A.
TITLE OF INVENTION: METHOD FOR DETECTING CANDIDA ALBICANS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burton Rodney
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/808,455A
FILING DATE: 19911217
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Boeden, James M.
REGISTRATION NUMBER: 32,962
REFERENCE/DOCKET NUMBER: GP65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 921-4163
TELEFAX: (609) 921-4526
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1747 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-808-455A-2

Query Match
Best Local Similarity 70.7%; Score 19.8; DB 1; Length 1747;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAAAAAGATGCGCAAGATATT 25
DB 704 AAAAAAAGATGCGCAAGATTTT 726

RESULT 9
Sequence 3, Application US/08455073A
Patent No. 5876949
GENERAL INFORMATION:
APPLICANT: Gideon Dreyfuss
APPLICANT: MIKIKO C. Stomi
APPLICANT: Yan Zhang
TITLE OF INVENTION: Fragile X Related Proteins, Compositions And Methods
TITLE OF INVENTION: Of Making And Using The Same
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5876949f1s
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,073A
```

```
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1863 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-455-073A-3

Query Match
Best Local Similarity 67.1%; Score 18.8; DB 2; Length 1863;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AAAAGATGCGCAAGATATTCAA 28
DB 894 AAAAAATGCGCAAGATTATCAA 915

RESULT 10
US-09-134-001C-2381
Sequence 2381, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: CTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2381
LENGTH: 2415
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2381

Query Match
Best Local Similarity 66.4%; Score 18.6; DB 4; Length 2415;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATT 25
DB 1203 AAATAAAAAGATGCTAAGATAAT 1227

RESULT 11
US-08-891-640-1/C
Sequence 1, Application US/08891640
Patent No. 6268173
GENERAL INFORMATION:
APPLICANT: Chambon, Pierre
APPLICANT: Gronemeyer, Hinfich
APPLICANT: Voegel, Johannes
APPLICANT: Lutz, Yves
TITLE OF INVENTION: Transcriptional Intermediary Factor-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
CITY: Washington
STATE: DC
```

COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,640
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,247
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1383.0130001/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6156 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 163..4554
US-08-891-640-1

Query Match 66.4%; Score 18.6; DB 4; Length 6156;
Best Local Similarity 84.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAGAGAAAAAGATGCGCAAGATATT 25
DB 5264 AAGAGAAAAACACGAAAAAATATT 5240

RESULT 12
US-09-723-535-3/C
Sequence 3, Application US/09723535
Patent No. 6355483
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-2 EXPRESSION
FILE REFERENCE: RTS-0225
CURRENT APPLICATION NUMBER: US/09/723,535
CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 3
LENGTH: 6156
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (163)..(4557)
US-09-723-535-3

Query Match 66.4%; Score 18.6; DB 4; Length 6156;
Best Local Similarity 84.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAGAGAAAAAGATGCGCAAGATATT 25
DB 5264 AAGAGAAAAACACGAAAAAATATT 5240

RESULT 13

US-08-737-298-1
Sequence 1, Application US/08737298
Patent No. 5910629
GENERAL INFORMATION:
APPLICANT: STRITTMAYER, Gunter
TITLE OF INVENTION: CHIMERIC GENES COMPRISING A
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,298
FILING DATE: 06-JAN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-121P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc. feature
LOCATION: 1..273
OTHER INFORMATION: /note="273 bp prp1-1 fragment,
OTHER INFORMATION: corresponding to position 402 to -130 of the prp1-1
OTHER INFORMATION: promoter (Martini et al., 1993)"
US-08-737-298-1

Query Match 65.7%; Score 18.4; DB 2; Length 273;
Best Local Similarity 78.6%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAGAGAAAAAGATGCGCAAGATATTCAA 28
DB 51 AAATTAATAATATGTCAAAATATTAA 78

RESULT 14
US-09-328-111-506
Sequence 506, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
APPLICANT: Endege, Willson O.
APPLICANT: Stohmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Dertl, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert


```

: TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
: FILE REFERENCE: CCD-257 (US)
: CURRENT APPLICATION NUMBER: US/09/328,111
: CURRENT FILING DATE: 1999-06-08
: EARLIER APPLICATION NUMBER: US 60/088,801
: EARLIER FILING DATE: 1998-06-10
: NUMBER OF SEQ ID NOS: 850
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 506
: LENGTH: 545
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(545)
: OTHER INFORMATION: n = A,T,C or G
: US-09-328-111-506

Query Match          65.7%; Score 18.4; DB 4; length 545;
Best Local Similarity 78.6%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 AAAGAAAAAAGATGCCAAGATATTCAA 28
    ||| ||| ||| ||| ||| ||| |||
DB 153 AAGCAAAAAAGACGCGAAAAATATACCA 180

RESULT 15
US-08-248-466B-6
: Sequence 6, Application US/08248466B
: Patent No. 5629182
: GENERAL INFORMATION:
: APPLICANT: CHOPIN, MARIE-CRISTINE
: APPLICANT: CUZEL, PIERRE-JEAN
: TITLE OF INVENTION: CLONING OF DNA FRAGMENTS ENCODING A
: TITLE OF INVENTION: MECHANISM FOR RESISTANCE TO BACTERIOPHAGES
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
: ADDRESSEE: P.C.
: STREET: 1755 S. Jefferson Davis Highway, Suite 400
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/248,466B
: FILING DATE: 24-MAY-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/988,959
: FILING DATE: 15-MAR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 90/11381
: FILING DATE: 14-SEP-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: OBLON, NO. 5629182man F.
: REGISTRATION NUMBER: 24,618
: REFERENCE/DOCKET NUMBER: 384-033-0 PCT FWC CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 413-3000
: TELEFAX: (703) 413-2220
: TELEX: 248855 OPAT UR
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1240 base pairs
: TYPE: nucleic acid
```

```

: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: -35_signal
: LOCATION: 33..38
: FEATURE:
: NAME/KEY: -10_signal
: LOCATION: 57..62
: FEATURE:
: NAME/KEY: RBS
: LOCATION: 133..137
: US-08-248-466B-6

Query Match          65.7%; Score 18.4; DB 1; length 1240;
Best Local Similarity 78.6%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 AAAGAAAAAAGATGCCAAGATATTCAA 28
    ||| ||| ||| ||| ||| ||| |||
DB 238 AAGAGATAAGATTCCAAAGATTAACCA 265
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Search completed: December 10, 2002, 22:54:35
Job time : 40.2926 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 ; Search time 1025.47 Seconds
(Without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579A-21
Perfect score: 20
Sequence: 1 gtaagtgatgatacttgc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
otal number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estbda:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
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6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_prod:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	90.0	543	14	BQ299830 QV1-KT002
C 2	17.4	87.0	197	9	AU036282 AU036282
C 3	17.4	87.0	622	10	BH761716 BMBAC374C
C 4	17.4	87.0	672	10	AV821890 AV821890
C 5	17	85.0	537	13	BM303591 SNEST461
C 6	17	85.0	722	17	BH468476 BOHRM34TF

Result No.	Score	Query Match	Length	DB ID	Description
C 7	17	85.0	812	17	BH588212 BOHB103TF
C 8	16.8	84.0	329	14	T75914
C 9	16.8	84.0	417	10	T45901
C 10	16.8	84.0	431	10	AV807336
C 11	16.8	84.0	618	13	BM077153
C 12	16.4	82.0	171	17	A2059099
C 13	16.4	82.0	393	13	A0492427
C 14	16.4	82.0	418	10	AW760469
C 15	16.4	82.0	425	17	BH320276
C 16	16.4	82.0	433	17	AO818960
C 17	16.4	82.0	467	10	AM634994
C 18	16.4	82.0	509	13	B1941756
C 19	16.4	82.0	567	17	BH767554
C 20	16.4	82.0	592	9	AT257715
C 21	16.4	82.0	592	17	AO250543
C 22	16.4	82.0	618	17	A2722668
C 23	16.4	82.0	693	9	A1975290
C 24	16.4	82.0	706	12	BF974745
C 25	16.4	82.0	720	9	AU234559
C 26	16.4	82.0	729	17	BH013591
C 27	16.4	82.0	858	12	BG742644
C 28	16	80.0	391	17	AO012704
C 29	16	80.0	478	17	AO338636
C 30	16	80.0	772	12	BG784784
C 31	16	80.0	801	17	BH488655
C 32	15.8	79.0	182	14	BQ513203
C 33	15.8	79.0	184	13	BJ518549
C 34	15.8	79.0	240	10	BM073140
C 35	15.8	79.0	275	17	A2696726
C 36	15.8	79.0	282	17	A2979689
C 37	15.8	79.0	293	9	AA531485
C 38	15.8	79.0	291	14	BQ370240
C 39	15.8	79.0	299	17	AO145901
C 40	15.8	79.0	318	17	AO067016
C 41	15.8	79.0	331	17	BH655762
C 42	15.8	79.0	365	9	AA163000
C 43	15.8	79.0	400	17	CNS00NG8
C 44	15.8	79.0	420	17	AL760169
C 45	15.8	79.0	423	17	AO434889

ALIGNMENTS

RESULT 1
LOCUS BQ299830/c
DEFINITION OVI-KT0023-131100-475-c07 KT0023 Homo sapiens CDNA, mRNA sequence.
ACCESSION BQ299830
VERSION BQ299830.1 GI:20815352
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 543)
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baita,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brenlanl,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL.
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=QV1&t2=QV1-KT0023-1311100-475-C07&t3=2000-11-13&t4=1>)
See RefSeq and its forward

ASE COUNT	164 a	114 c	101 g	164 t
ORIGIN				

RESULT 2	
AU036282/c	
LOCUS	
DEFINITION	
AU036282	197 bp
AU036282	polyandrocampa misakiensis white spot budding stage
polyandrocampa misakiensis cDNA, mRNA sequence.	
LOCATION	
EST 29-SEP-1999	

BASE COUNT	55 a	31 c	36 g	75 t
ORIGIN				

Oy	1	GTTAGTTGAATATCTTGC	19
			1
Db	43	GTTAGTTGAATATCTTAC	25

RESULT 3	BH761716/c	622 bp	DNA	linear	GSS 20-MAR-2002
LOCUS	BH761716/c				
DEFINITION	BH761716 BHAC3224G04T_PSU Brugia malayi Genomic Bac Library 3 Brugia malayi genomic, DNA sequence.				
ACCESSION	BH761716				
VERSION	BH761716.1				
KEYWORDS	GI:1955979				
SOURCE	GSS. Brugia malayi.				
ORGANISM	Brugia malayi.				

BASE COUNT	200 a	83 c	106 g	233 t
ORIGIN				

RESULT	4
AV821890/c	
LOCUS	672 bp mRNA linear EST 01-APR-2002
DEFINITION	Arabidopsis thaliana cDNA clone RAFL04-17-K09 5'
	mRNA sequence.
ACCESSION	AV821890
VERSION	AV821890.1 GI:19863921

KEYWORDS EST.
SOURCE Chale cress.
ORGANISM Arabidopsis thaliana
REFERENCE Arabidopsis thaliana
AUTHORS Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 672)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Saito, M., Nakajima, M.,
Omori, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, T.,
Arikawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified Bluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/Plant/index_e.html) for
further details.
FEATURES
Location/Qualifiers
1..672
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAF104-17-K09"
/clone_lib="RAF14"
/dev_stage="roselte plants"
/lab_host="SOLR"
/note="Site_1: SstI; Site_2: XhoI; subjected to
cold-treated(1.2,5,10,24 hr)"
BASE COUNT 209 a 124 c 165 g 174 t
ORIGIN
Query Match 87.0%; Score 17.4; DB 10; Length 672;
Best Local Similarity 94.7%; Pred. No. 5,1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TTACTGATATCTTGGC 20
1 ||||||||||||||||
Db 383 TGAGTTGAATCTTTGCC 365
RESULT 5
3M303591/c 537 bp mRNA linear EST 02-JAN-2002
DEFINITION SNEST461111.y1 csn 1 S neurona invitro merizoite cDNA Sarcocystis
neurona cDNA 5', mRNA sequence.
ACCESSION BM303591
VERSION BM303591.1 GI:18035295
KEYWORDS EST.
SOURCE Sarcocystis neurona.
ORGANISM Sarcocystis neurona.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Sarcocystis.
REFERENCE 1 (bases 1 to 537)
Howe, D.K., Stamper, S., Tang, K., Sibley, L.D., Clifton, S., Marra, M.,
Hillier, L., Pape, D., Martin, J., Wylie, T., Thelais, B., Bowers, Y.,
Gibbons, M., Ritter, E., McCann, R., Birstein, A., Bennett, J., Schmitt,
A., Ronko, I., Tsagareishvili, R., Fedele, M., Belaygorod, L.,
Franklin, C., Carr, L.M., Grow, A., Maguire, L., Wadkins, J., Ritchey, J.,
Waterson, R. and Wilson, R.
Sarcocystis neurona EST project
Unpublished (2000)
Contact: Daniel K. Howe
Sarcocystis neurona EST project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
TITLE
JOURNAL
COMMENT

Fax: 314 286 1810
Email: estevenson.wustl.edu
Contact Daniel K. Howe (dkhowe2@pop.uky.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -408P from Gluco
High quality sequence stop: 421.
FEATURES
Location/Qualifiers
1..537
/organism="Sarcocystis neurona"
/strain="Sn3"
/db_xref="taxon:42890"
/clone_lib="csn 1 S neurona invitro merozoite cDNA"
/dev_stage="merozoite"
/lab_host="DH10B"
/note="Vector: phuescript SK-; Site_1: KccOI; Site_2:
XhoI; The library was constructed by Dan Howe, University
of Kentucky. cDNAs were synthesized from poly(A)+ RNA
by oligo d(T) priming and directionally cloned into the
Uni-ZAP XR lambda vector. The library was mass excised
as phagemids and rescued in SOLR cells. The plasmid
library was recovered from the SOLR cells and transformed
in mass into DH10B cells for sequencing. WARNING: the
library contains a small percentage of cDNAs derived from
the bovine host cells."
BASE COUNT 129 a 129 c 139 g 140 t
ORIGIN
Query Match 85.0%; Score 17; DB 13; Length 537;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ACTTGAAATATCTTGGC 20
1 ||||||||||||||||
Db 149 ACTTGAAATATCTTGGC 133
RESULT 6
BH468476 722 bp DNA linear GSS 13-DEC-2001
LOCUS BOHRM34TF BOHR Brassica oleracea genomic clone BOHRM34, DNA
DEFINITION Sequence.
ACCESSION BH468476
VERSION BH468476.1 GI:17673478
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 722)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOHRM34TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
FEATURES
Location/Qualifiers
1..722
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHRM34"
/clone_lib="BOHR"
/note="Vector: PHOSI; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHOSI using BstXI linkers"
BASE COUNT 285 a 109 c 103 g 225 t

ORIGIN

Query Match 85.0%; Score 17; DB 17; Length 722;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTACGTGATATCTTT 17
 |||||||
 Db 533 GTTAGTTGAATATCTTT 549

RESULT 7
 BH588212/c 812 bp DNA linear GSS 15-DEC-2001
 LOCUS BOHB103TF BOHB Brassica oleracea genomic clone BOHB103, DNA
 DEFINITION sequence.
 ACCESSION BH588212
 VERSION BH588212.1 GI:17840670
 KEYWORDS GSS.
 SOURCE Brassica oleracea.
 ORGANISM Brassica oleracea.

REFERENCE
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdlowne@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TP
 Class: Sheared ends.
 Location/Qualifiers
 1. 812
 /organism="Brassica oleracea"
 /strain="T01000DH3"
 /db_xref="taxon:3712"
 /clone="BOHB103"
 /clone_1lb="BOHB"
 /note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

BASE COUNT 263 a 205 c 136 g 208 t

ORIGIN

Query Match 85.0%; Score 17; DB 17; Length 812;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TTAGTTGATATCTTTG 18
 |||||||
 Db 37 TTAGTTGAATATCTTTG 21

RESULT 8
 T75914/c 329 bp mRNA linear EST 09-JAN-1998
 LOCUS 10692 Lambda-PRL2 Arabidopsis thaliana cDNA clone 148D147, mRNA
 DEFINITION sequence.
 ACCESSION T75914
 VERSION T75914.1 GI:934966
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana

REFERENCE
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 329)

AUTHORS Newman,T., debruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.

TITLE Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones

JOURNAL Plant Physiol. 106, 1241-1255 (1994)

MEDLINE 95148729

COMMENT On Apr 14, 1993 this sequence version replaced gi:692676.
 Contact: Thomas Newman
 MSU-DOE Plant Research Laboratory
 Michigan State University
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI
 Tel: 517-353-0854
 Fax: 517-353-9168
 Email: 22313c@eddm.cl.msu.edu
 Seq primer: T7 dye primer.
 Location/Qualifiers
 1. 329
 /organism="Arabidopsis thaliana"
 /strain="var columbia"
 /db_xref="taxon:3702"
 /clone="148D147"
 /clone_1lb="Lambda-PRL2"
 /note="Vector: lambda Z1p-10x; Site_1: Sal; Site_2: Not; lambda PRL2 is a cDNA library derived from equal quantiles of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Z1p-10x. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA."

BASE COUNT 104 a 45 c 73 g 97 t 10 others

ORIGIN

Query Match 84.0%; Score 16.8; DB 14; Length 329;
 Best Local Similarity 90.0%; Pred. No. 8.9e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTTACGTGATATCTTCCC 20
 |||||||
 Db 59 GTTAGTTGAACATCTTGCC 40

RESULT 9
 T45901/c 417 bp mRNA linear EST 04-AUG-1998
 LOCUS 9164 Lambda-PRL2 Arabidopsis thaliana cDNA clone 133J247, mRNA
 DEFINITION sequence.
 ACCESSION T45901
 VERSION T45901.1 GI:2762614
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana

REFERENCE
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 417)
 Newman,T., debruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.

TITLE Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones

JOURNAL Plant Physiol. 106, 1241-1255 (1994)

MEDLINE 95148729

COMMENT On Jan 9, 1998 this sequence version replaced gi:934153.
 Contact: Thomas Newman
 MSU-DOE Plant Research Laboratory
 Michigan State University
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI

Tel: 517-353-0854
 Fax: 517-353-9168
 Email: 22313tcn@dm.c1.msu.edu
 Seq primer: T7 dye primer.

FEATURES
 source
 Location/Qualifiers

1. 417
 /organism="Arabidopsis thaliana"
 /strain="var columbiana"
 /db_xref="taxon:3702"

Query Match 84.0% Score 16.8; DB 14; Length 417;
 Best Local Similarity 90.0% Pred. No. 9.2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GTTACTGCAATATCTTGCC 20
 ||| ||||| ||||| |||||
 Db 307 GTTGCTGACATCTTGCC 288
 BASE COUNT 135 a 62 c 112 g 92 t 16 others
 ORIGIN

/note="Vector: lambda Z1p-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle; half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRL's lambda Z1p-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA."

RESULT 10 431 bp mRNA linear EST 29-MAR-2002
 AV807336
 LOCUS AV807336 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-49-P22 3',
 DEFINITION mRNA sequence.

ACCESSION AV807336
 VERSION AV807336.1 GI:19841321
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae, eurosids 11; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 431)

SEKI, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Atakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.

Large scale analysis of Arabidopsis full-length cDNA (2002b)
 Unpublished (2002)

COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060

FEATURES
 source
 Location/Qualifiers
 1. 431
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /clone="RAFL09-49-P22"
 /clone_lib="RAFL9"

/dev_stage="plants at various developmental stages from germination to mature seeds"
 /lab_host="DH10B"
 /note="Site_1: BamHI; Site_2: SalI; subjected to denaturation (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"

BASE COUNT 132 a 99 c 68 g 132 t
 ORIGIN

Query Match 84.0% Score 16.8; DB 10; Length 431;
 Best Local Similarity 90.0% Pred. No. 9.2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTTACTGCAATATCTTGCC 20
 ||| ||||| ||||| |||||
 Db 303 GTTGCTGACATCTTGCC 322

RESULT 11 618 bp mRNA linear EST 05-FEB-2002
 BM077153
 LOCUS BM077153
 DEFINITION TREST-A0283 Hypocrea jecorina cDNA clone TREST-A0283 5', mRNA sequence.

ACCESSION BM077153
 VERSION BM077153.1 GI:18498335
 KEYWORDS EST.
 SOURCE Hypocrea jecorina.
 ORGANISM Hypocrea jecorina
 Eukaryota: Fungi: Ascomycota: Pezizomycotina: Sordariomycetes: Hypocreales: Hypocreaceae: Hypocrea.

REFERENCE 1 (bases 1 to 618)
 Chamberg, F.S., Bonaccorsi, E.D., Ferreira, A.J.S., Ramos, A.S.P., Ferreira, J.R.Jr., Abraham-Neto, J., Parah, J.P.S. and El-Dorri, H. Elucidation of the metabolic fate of glucose in the filamentous fungus Trichoderma reesei using expressed sequence tag (EST) analysis and cDNA microarrays

J Biol Chem. 277 (16), 13983-13988 (2002)
 JOURNAL MEDLINE
 COMMENT Contact: El Dorri, Hamza
 Department of Biochemistry
 Institute of Chemistry
 Avenida Professor Lineu Prestes, 748, Sao Paulo, SP, 05508-900, BRASIL

Tel: (55) 11-38183848
 Fax: (55) 11-38183848
 Email: dorrie@iq.usp.br
 PCR Primers
 FORWARD: Universal M13 forward primer
 BACKWARD: Universal M13 reverse primer
 Plate: 3 row: H column: 7
 Seq primer: M13 reverse primer
 High quality sequence stop: 618
 POLYA-No.

FEATURES
 source
 Location/Qualifiers
 1. 618
 /organism="Hypocrea jecorina"
 /strain="QM9414 (ATCC26921)"
 /db_xref="taxon:51453"
 /clone="TREST-A"
 /clone_lib="TREST-A"
 /sex="Asexual"
 /issue_type="Mycelia"
 /dev_stage="18 hr glycerol-grown culture"
 /lab_host="E. coli SOLR cells (kanamycin resistant)"
 /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; anamorph-trichoderma reesei; Cloned unidirectionally, 5' end of the cDNA cloned into EcoRI site of pBluescript. Primer: Oligo (dT). Average insert size: 1,2 kb; Uni-ZAP XR Vector system -5' adaptor sequence: 5'-GAATTCGACGACGAG3' -3' adaptor sequence: 5'-CTCCAGCTTTTCTTTTCTTTTCTTTT3''

BASE COUNT 108 a 176 c 162 g 172 t
 ORIGIN

Query Match 84.0%; Score 16.8; DB 13; Length 618;
 Best Local Similarity 90.0%; Pred. No. 9,6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTTACTGTAATATCTTTG 20
 ||||||| ||| |||||
 DB 75 GTTACTGTAATATCTTTG 94

RESULT 12
 A2059099 171 bp DNA linear GSS 30-MAR-2000
 LOCUS RPCI-23-426115.TJ RPCI-23 Mus musculus genomic clone RPCI-23-426115
 DEFINITION DNA sequence.
 ACCESSION A2059099
 VERSION A2059099.1 GI:7350336
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 171)
 Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akturet,
 B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
 and Fraser,C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other GSS: RPCI-23-426115.TV
 TITLE
 JOURNAL
 COMMENT

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Libraries are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieter@edjlong.med.buhalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buhalo.edu/orderingframe.htm)
 or from Resea ch Genetics (info@resgen.com). BAC end page:
 http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
 plate: 426 row: I column: 15
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source location/Qualifiers

1..171
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-426115"
 /clone.lib="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site_1:
 EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Size
 selected DNA was cloned into the pBAC3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 40 a 31 c 29 g 71 t
 ORIGIN

Query Match 82.0%; Score 16.4; DB 17; Length 171;
 Best Local Similarity 94.4%; Pred. No. 1.3e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTACTGTAATATCTTTG 18
 ||||||| ||| |||||
 DB 24 GTTACTGTAATATCTTTG 41

RESULT 13
 A0492427 393 bp DNA linear GSS 28-APR-1999
 LOCUS HS_5143_B2.D11-SP6E RPCI-11 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate=719 Col=22 Row=H, DNA sequence.
 ACCESSION A0492427
 VERSION A0492427.1 GI:4691915
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 393)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 99380589
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@edjlong.med.buhalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buhalo.edu/ordering_bac.htm)
 or from Resear h Genetics (info@resgen.com). BAC end Web Server:
 http://www.htsc.washington.edu
 plate: 719 row: H column: 22
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 393.

FEATURES
 source location/Qualifiers

1..393
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=719 Col=22 Row=H"
 /clone.lib="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBAC3.6 vector at EcoRI sites"
 BASE COUNT 109 a 59 c 69 g 152 t 4 others
 ORIGIN

Query Match 82.0%; Score 16.4; DB 17; Length 393;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTACTGTAATATCTTTG 18
 ||||||| ||| |||||
 DB 37 GTTACTGTAATATCTTTG 54

RESULT 14
 A0760469 418 bp mRNA linear EST 03-DEC-2001
 LOCUS s150g04.y1 gm-cl027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION gm-cl027-4783 5', similar to SW:R32_MEDSA P11105 HISTONE H3.2,
 MINOR. [3] SW:R32_MEDSA TR:Q43202 ;, mRNA sequence.
 ACCESSION A0760469
 VERSION A0760469.1 GI:7692361
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine (bases 1 to 418)

REFERENCE

Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corryell, V., Khanna

, A., Holla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Rheising, B., Allen, M., Bowers

, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
R., Rittler, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann

, R., Waterston, R. and Wilson, R.
Public Soybean EST Project

Unpublished (1999)
Contact: Shoemaker R./Public Soybean EST Project

Public Soybean EST Project
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert length: 655 Std Error: 0.00

High quality sequence stop: 331.

FEATURES

Location/Qualifiers

1..418

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl027-4783"

/clone_1lb="Gm-cl027"

/tissue_type="cotyledons of 3- and 7-day-old Williams

seedlings"

/lab_host="DH10B"

/note="Vector: Bluescript II SK+; Site-1: EcoRI; Site-2:
XhoI; This cDNA library was constructed from mRNA isolated

from cotyledons of 3- and 7-day-old Williams seedlings
which were propagated on paper towels in distilled

water. The cotyledons were flash-frozen in liquid
nitrogen, then lyophilized for 72 hours. Unequal amounts

of mRNA was used for cDNA synthesis. Stratagene's cDNA
Synthex Kit (catalog number 200401) was used to

synthesize the cDNA. First-strand synthesis was
performed with 5-methyl dCTP, hence the ligated cDNA was

hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An anchor

nucleotide (V=A, C, or G) was added to the 3' end of the
primer (GAGAGAGAGAGAGAGAGACTACTGAG(TT)18) to anchor

the primer at the 5' end of the poly(A) tract. After
second-strand synthesis, the cDNA ends were filled in

with cloned Pfu DNA, ligated to EcoRI adapters and
subsequently phosphorylated. The XhoI site within the

first-strand synthesis primer was then restricted by
digestion with XhoI; all XhoI sites in the cDNA would be

protected by their hemimethylated status. The cDNA
constructs were size-fractionated with a 500 bp cutoff,

using GibcoBRL Life Technologies' cDNA Size Fractionation
column. The column eluent was then ligated into

Stratagene's Bluescript(lm) II XR predigested vector
(pBluescript II SK(+)) that has been digested with EcoRI

and XhoI, and phosphorylated by Stratagene). 97% of the
white and blue colonies appear to contain recombinant

plasmids with cDNA inserts, based on size (n=30). This
library was constructed by Dr. Paul Kelm and Dr. Virginia

Corryell."

BASE COUNT 141 a 107 c 73 g 96 t 1 others
ORIGIN

Query Match 82.0%; Score 16.4; DB 10; Length 418;

Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTACTGAAATCTTTC 18
|||||

Db 393 GTTACTGAAATCTTTC 376

RESULT 15

BH320276

LOCUS

DEFINITION

CH230-196P16.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone

CH230-196P16, DNA sequence.

VERSION

BH320276

KEYWORDS

BH320276.1 GI:17250990

SSS.

SOURCE

ORGANISM

Rattus norvegicus

Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

(bases 1 to 425)

REFERENCE

AUTHORS

Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn

, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de

Jong, P. and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment

Unpublished (1999)

Other GSSs: CH230-196P16.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@tigr.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering_information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

Plate: 196 row: P column: 16

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..425

/organism="Rattus norvegicus"

/strain="BN/SSNhd/MCw"

/db_xref="taxon:10116"

/clone="CH230-196P16"

/clone_1lb="CHORI-230 Segment 1"

/sex="Female"

/cell_type="Brain"

/note="Vector: pTARBAC2.1; Site-1: EcoRI; Site-2: EcoRI;

CHORI-230 Rat (BN/SSNhd/MCw) BAC library produced by

Pieter de Jong"

BASE COUNT 66 a 76 c 60 g 223 t

ORIGIN

Query Match 82.0%; Score 16.4; DB 17; Length 425;

Best Local Similarity 94.4%; Pred. No. 1.4e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTACTGAAATCTTTC 19

|||||

Db 61 TTATTGAAATCTTTC 78

Search completed: December 10, 2002, 22:50:00
Job time : 1030.47 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 ; Search time 607.084 Seconds

(without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579a-22

Perfect score: 28

Sequence: 1 aagaagaaagatgcaagatattcaa 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

otal number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
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6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
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16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
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23: em_pat: *
24: em_ph: *
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26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hlg_hum: *
31: em_hlg_inv: *
32: em_hlg_other: *
33: em_hlg_mus: *
34: em_hlg_pln: *
35: em_hlg_rod: *
36: em_hlg_mam: *
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38: em_sy: *
39: em_higo_hum: *
40: em_higo_mus: *
41: em_higo_other: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	28	100.0	28	6	AX306863	AX306863 Sequence
2	28	100.0	39	6	AX306869	AX306869 Sequence
3	28	100.0	1789	6	E09772	E09772 The base se
4	28	100.0	2007	6	AR089410	AR089410 Sequence
5	28	100.0	2007	6	AR093610	AR093610 Sequence
6	28	100.0	2332	1	SABBP	Y00688 Staphylococ
7	28	100.0	2332	6	E03736	E03736 DNA sequenc
8	28	100.0	2454	1	SEMECAPB	X52592 S. epidermi
9	28	100.0	2455	6	E09771	E09771 The base se
10	28	100.0	2456	1	SAMECAPB	X52593 S. aureus m
11	28	100.0	2456	6	AX110445	AX110445 Sequence
12	28	100.0	5596	1	SSK8MECA	Y13096 S.sciuri me
13	28	100.0	6368	1	SSK3MECA2	Y14051 Staphylococ
14	28	100.0	9047	1	SAMECAR1	AB063173 Staphyloc
15	28	100.0	21777	1	AB063173	AB063172 Staphyloc
16	28	100.0	26030	1	AB063172	AB063173 Staphyloc
17	28	100.0	39332	1	AB033763	D86934 Staphylococ
18	28	100.0	58237	1	D86934	AB033767 Staphyloc
19	28	100.0	68256	1	AB037671	AP004822 Staphyloc
20	28	100.0	290250	1	AP004822	AP003129 Staphyloc
21	28	100.0	298050	1	AP003129	AP003358 Staphyloc
22	28	100.0	349999	1	AP003358	Y13052 S.sciuri me
23	26.4	94.3	5806	1	SSK3MECA1	Y13023 S.sciuri me
24	23.2	82.9	5068	1	SSK1MECA	Y13094 S.sciuri me
25	23.2	82.9	6684	1	SSK1MECA	Y158820 Homo sapi
26	23.2	82.9	109792	2	AL158820	AL121867 Human DNA
27	23.2	82.9	131238	9	HS405021	AL121673 Human DNA
28	23.2	82.9	151163	9	HS405022	AC099414 Mus muscu
29	23.2	82.9	243457	2	AC099414	AC022730 Homo sapi
30	22.4	80.0	153468	9	AC022730	AP004516 Lotus jap
31	22.2	79.3	20786	8	AP004516	AL158034 Homo sapi
32	22.2	79.3	150728	2	AL158034	AC079856 Homo sapi
33	22.2	79.3	155340	9	AC079856	AC093212 Homo sapi
34	22.2	79.3	164598	2	AC093212	AC022448 Homo sapi
35	22.2	79.3	165434	9	AC022448	AC110078 Homo sapi
36	22.2	79.3	196117	2	AC110078	AC018872 Homo sapi
37	22.2	79.3	201340	8	PD088230	U88230 Puccinia dr
38	21.8	77.9	624	2	AC129656	AC095513 Homo sapi
39	21.8	77.9	151389	9	AC095513	AC129656 Rattus no
40	21.6	77.1	170931	2	AC090352	AC090352 Homo sapi
41	21.6	77.1	33446	2	AC102773	AC102773 Mus muscu
42	21.6	77.1	64102	2	AC102773	AC005009 Homo sapi
43	21.6	77.1	71235	9	AC005009	AL772369 Human DNA
44	21.6	77.1	71591	9	AL772369	AL136145 Human DNA
45	21.6	77.1	83809	9	AL136145	

ALIGNMENTS

RESULT 1	AX306863	28 bp	DNA	linear	PAT 14-DEC-2001
LOCUS	AX306863				
DEFINITION	Sequence 22 from Patent EP1160333.				
ACCESSION	AX306863				
VERSION	AX306863.1 GI:117894685				
KEYWORDS					
SOURCE	synthetic construct.				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Taya, T., Ishiguro, T. and Saito, J.				
TITLE	Oligonucleotides and method for detection of meca gene of methicillin-resistant Staphylococcus aureus				
JOURNAL	Patent: EP 1160333-A 22 05-DEC-2001;				

FEATURES
source
Tosoh Corporation (JP)
Location/Qualifiers
1..28
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT
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Best Local Similarity 100.0%; Score 28; DB 6; Length 28;
Pred. No. 6.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGAGAAAAAGATGCCAAGATATTCAA 28
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Db 1 AAGAGAAAAAGATGCCAAGATATTCAA 28

RESULT 2
AX306869/c
LOCUS AX306869 39 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 28 from Patent EP1160333.
ACCESSION AX306869
VERSION AX306869.1 GI:17894691
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE
AUTHORS Taya,T., Ishiguro,T. and Saito,J.
TITLE Oligonucleotides and method for detection of meca gene of
JOURNAL methicillin-resistant Staphylococcus aureus
Tosoh Corporation (JP)
LOCATION/Qualifiers

FEATURES
source 1..39
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Probe"

BASE COUNT
5 a 7 c 4 g 23 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 28; DB 6; Length 39;
Pred. No. 6.2;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGAGAAAAAGATGCCAAGATATTCAA 28
|||||
Db 33 AAGAGAAAAAGATGCCAAGATATTCAA 6

RESULT 3
E09772
LOCUS E09772 1789 bp RNA linear PAT 29-SEP-1997
DEFINITION The base sequence of modified meca DNA.
ACCESSION E09772
VERSION E09772.1 GI:22026401
KEYWORDS JP 1995209294-A/2.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
1 (bases 1 to 1789)
Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.
NOVEL 'MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
Patent: JP 1995209294-A 2, 11-AUG-1995:
JOURNAL KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/2
PD 11-AUG-1995
PI 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
MASAHISA.

PI SUGURO KAZUYA
PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC
C12R1:19),
PC (C12P21/02,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH FT source 1..1789
FT FT /organism="Staphylococcus aureus" FT CDS
FT 1..1608 /product="Modified meca".
FEATURES
source FT
Location/Qualifiers
1..1789
/organism="Staphylococcus aureus"
/db_xref="taxon:1280"

BASE COUNT
735 a 263 c 302 g 489 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 28; DB 6; Length 1789;
Pred. No. 4.2;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGAGAAAAAGATGCCAAGATATTCAA 28
|||||
Db 549 AAGAGAAAAAGATGCCAAGATATTCAA 576

RESULT 4
AR089410
LOCUS AR089410 2007 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 169 from patent US 5994066.
ACCESSION AR089410
VERSION AR089410.1 GI:10016167
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 2007)
TITLE Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.
Species-specific and universal DNA probes and amplification primers
to rapidly detect and identify common bacterial pathogens and
associated antibiotic resistance genes from clinical specimens for
routine diagnosis in microbiology laboratories
JOURNAL Patent: US 5994066-A 169 30-NOV-1999:
LOCATION/Qualifiers

FEATURES
source 1..2007
/organism="unknown"

BASE COUNT
855 a 270 c 341 g 541 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 28; DB 6; Length 2007;
Pred. No. 4.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGAGAAAAAGATGCCAAGATATTCAA 28
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Db 948 AAGAGAAAAAGATGCCAAGATATTCAA 975

RESULT 5
AR093610
LOCUS AR093610 2007 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 169 from patent US 6001564.
ACCESSION AR093610
VERSION AR093610.1 GI:10020359
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 2007)
Bergeron,M.G., Ouellette,M. and Roy,P.H.
Species specific and universal DNA probes and amplification primers

to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
Patent: US 6001564-A 169 14-DEC-1999;

JOURNAL

source
Location/Qualifiers

BASE COUNT 855 a 270 c 341 g 541 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGAAAAAGATGCCAAGATATTCAA 28
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DB 948 AAGAAAAAGATGCCAAGATATTCAA 975

RESULT 6

APBP 2322 bp DNA linear BCT 12-SEP-1993

LOCUS Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible
DEFINITION penicillin-binding protein.
VERSION Y00688.1 GI:46628

KEYWORDS penicillin-binding protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.

REFERENCE 1 (bases 1 to 2322)
Authors Song, M.D., Machi, M., Doi, M., Ishino, F. and Matsubashi, M.

JOURNAL Evolution of an inducible penicillin-target protein in
MEDLINE methicillin-resistant Staphylococcus aureus by gene fusion
PUBMED FEMS Lett. 221 (1), 167-171 (1987)
87304805
3305073

REFERENCE 2 (bases 1 to 2322)
Authors Kyffel, C., Tesch, W., Birch-Machin, I., Reynolds, P.F.,
Barberis-Maino, L., Kayser, F.H. and Berger-Bachli, B.

JOURNAL Sequence comparison of mecA genes isolated from
MEDLINE methicillin-resistant Staphylococcus aureus and Staphylococcus
PUBMED epidermidis
91033056
2227446

FEATURES
AUTHORS Data kindly reviewed (13.1.88) by Matsubashi.
LOCATION/Qualifiers
1..2322

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/db_xref="taxon:1280"
1..2013
/note="penicillin-binding protein (AA 1-670)"
/codon_start=1
/transl_table=1
/protein_id="CAA68684.1"
/db_xref="GI:46629"
/db_xref="SWISS-PROT:P07944"

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TNGGIDNRNVGFNEVEKEDGMKLDMDHSVILPGMKDSDIHENLKSERGLDNRNV
ELANTGTHMRGLGIPKRVNSKDYKAIAELISDEYINNMKIKGYKMPHFETVK
KMDVGLSDPAKFKPLTTNETSRNPLCKASHLIGYVCPINSEELKQEKYKDDA
VIGKKGLFKIDKKLOHEDGYRTTVRVDDNSNTTAHTLIEKKKDGODIOLTDAYK
OKSIYNMKNNDYSGCTAIHPOTGELLAVTSPSYVYPPMYGMSMEYVNTLTDKKEP
LLNKFOITTSRSTOKITAMIGLNKTLTDKTSKIKTGCKQKSKSGYVNTREY
VNGNTDLKQALSSDNIFPARVAELGSKKKEGKKLGVGEDIPDTPYNAOISNK
NLDENLADSGYGGGELLINVOILSTYSALENNGINAPHLIDTNKTKWKNTIIS
KENINILNDGMOQVYVNTKHEIDYRSYVNLIGKSGTALMKMGCTGQIOGIFSYDK
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BASE COUNT 940 a 324 c 389 g 669 t
ORIGIN

Query Match 100.0%; Score 28; DB 1; Length 2322;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGAAAAAGATGCCAAGATATTCAA 28
|||||

DB 954 AAGAAAAAGATGCCAAGATATTCAA 981

RESULT 7

LOCUS E03736

DEFINITION DNA sequence of PBP2' gene for determination of methicillin
resistance.
VERSION E03736.1 GI:2171951

KEYWORDS JP 1992169200-A/9.
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 2322)

AUTHORS Watanabe, Y., Nakamura, E., Teraoka, H., Wada, K., Minamide, W. and
Murakami, K.

JOURNAL DETECTION OF PBP 2' GENE AND JUDGEMENT OF METHICILLIN RESISTANCE
Patent: JP 1992169200-A 9 17-JUN-1992;
SHIONOGI & CO LTD

COMMENT OS (methicillin resistant)staphylococcus aureus
PN JP 1992169200-A/9
PD 17-JUN-1992
PE 31-OCT-1990 JP 1990296708
PI WATANABE YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI,
MINAMIDE MAKIYO, MURAKAMI KAZUHIISA

PC C1201/68.C12N15/11;
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key
FT misc-feature 1..2322
FT /note="PBP2' gene for determination of FT
methicillin resistance".

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source Location/Qualifiers
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/db_xref="taxon:32644"

BASE COUNT 939 a 324 c 390 g 669 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2322;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGAAAAAGATGCCAAGATATTCAA 28
|||||

DB 954 AAGAAAAAGATGCCAAGATATTCAA 981

RESULT 8
SEMECAPB 2454 bp DNA linear BCT 12-SEP-1993

LOCUS S. epidermidis

DEFINITION S. epidermidis mecA gene for PBP2' (penicillin binding protein 2').
ACCESSION X52592
VERSION X52592.1 GI:46993

KEYWORDS mecA gene; methicillin resistance; penicillin-binding protein;
penicillin-binding protein 2'.
SOURCE Staphylococcus epidermidis.
ORGANISM Staphylococcus epidermidis

REFERENCE 1 (bases 1 to 2448)
Authors Kyffel, C.

TITLE Direct Submission

JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland

REFERENCE 2 (bases 1 to 2454)

AUTHORS Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E., Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.

TITLE Sequence comparison of meca genes from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis

JOURNAL 3 (bases 1 to 2454)

REFERENCE Gene (1990) In press

AUTHORS Ryffel,C.

TITLE Direct Submission

JOURNAL Submitted (23-JUL-1990) Ryffel C., University of Zuerich, Inst of Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland

REFERENCE 4 (bases 1 to 2454)

AUTHORS Ryffel,C., Tesch,W., Birch-Machin,I., Reynolds,P.E., Barberis-Maino,L., Kayser,F.H. and Berger-Bachli,B.

TITLE Sequence comparison of meca genes isolated from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis

JOURNAL Gene 94 (1), 137-138 (1990)

MEDLINE 91033056

PUBMED 2227446

COMMENT See also <X52593-4> and <Y00688>.

FEATURES

source Data kindly reviewed (23-JUL-1990) by C. Ryffel.

1. .2454
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101..105
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130..134
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VICKKGLKLYDKKLOHEDGYRVTYVDNSNTAHLTKKKKDKGKDLOTTDAKQK
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NFKVITTSRSTOKILTAMTGLNNKTLDDTSYKIDGKGMQKSKSGVNVTRYEVN
GNIDIKOALISSDNIPFARVALELGSKEKMKLGVEDIPSDYFVNAOISNNL
DNELIADSGYGGGELINPVQILSTYSALENNGNINAPHLKDTFNKWKNNISK
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441..448
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641..643
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652..653
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731..733
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780..781
/note="ct was ctt in [1]"
/citation-[1]
997 a 345 c 398 g 714 t

ORIGIN

Query Match 100.0%; Score 28; DB 1; Length 2454;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1088 AAGAAAAAAGATGCGCAAGATATTCAA 1115

RESULT 9

LOCUS E09771 2455 bp RNA linear PAT 29-SEP-1997

DEFINITION The base sequence of meca DNA.

ACCESSION E09771

VERSION E09771.1 GI:22026400

KEYWORDS JP 1995209294-A/1.

SOURCE Staphylococcus aureus.

ORGANISM Staphylococcus aureus

REFERENCE 1 (bases 1 to 2455)

AUTHORS Bacteria: Firmicutes; Bacillales; Staphylococcus.

TITLE Kono,M., Hiramatsu,K., Sasazu,M., Noguchi,M. and Suguro,K.

JOURNAL NOVEL 'MECA' PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS

Patent: JP 1995209294-A 1 11-AUG-1995;

OS KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD

PN JP 1995209294-A/1

PD 11-AUG-1995

PP 10-JAN-1994 JP 1994012226

PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI MASAHISA,

PI SUGURO KAZUYA

PC G01N33/53.C07K14/31.C12N1/21.C12N15/09.C12P21/02.C12N1/21. PC C12R1:19).

CC (C12P21/02.C12R1:19);

CC strandedness: Double;

CC topology: Linear;

FT Key location/Qualifiers

FT source 1..2455 /organism="Staphylococcus aureus" FT CDS

FT 134..2146 /product="meca protein".

FEATURES

source location/Qualifiers

1..2455 /organism="Staphylococcus aureus"

/db_xref="taxon:1280"

BASE COUNT 997 a 344 c 401 g 713 t

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2455;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1087 AAGAAAAAAGATGCGCAAGATATTCAA 1114

RESULT 10

LOCUS SAMECAPB 2456 bp DNA linear BCT 12-SEP-1993

DEFINITION S. aureus meca gene for PBP2' (penicillin binding protein 2').

ACCESSION X52593

VERSION X52593.1 GI:46610

KEYWORDS meca gene; methicillin resistance; penicillin-binding protein;

SOURCE Staphylococcus aureus.

ORGANISM Staphylococcus aureus

REFERENCE 1 (bases 1 to 2456)

AUTHORS Ryffel, C.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
 REFERENCE 2 (bases 1 to 2456)
 AUTHORS Ryffel, C., Tesch, W., Birch-Machlin, I., Reynolds, P.E., Barberis-Maino, L., Kayser, F.H. and Berger-Bach, B.
 TITLE Sequence comparison of meca genes isolated from methicillin-resistant Staphylococcus aureus and Staphylococcus epidermidis
 JOURNAL Gene 94 (1), 137-138 (1990)
 MEDLINE 91033056
 PUBMED 2227446
 COMMENT See also <X52592> and <X00688>.
 DATA kindly reviewed (23-JUL-1990) by C. Ryffel.
 FEATURES
 Source
 Location/Qualifiers
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 130..134
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 141..2147
 /note="PBP2" (AA 1-668)
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 Db 1088 AAGAGAAAAAGATGCCAAGATATTCAA 1115
 RESULT 11
 LOCUS AX110445 2456 bp DNA linear PAT 30-APR-2001
 DEFINITION Sequence 1178 from Patent WO0123604.
 ACCESSION AX110445
 VERSION AX110445.1 GI:13926737
 KEYWORDS
 ORGANISM Staphylococcus aureus subsp. aureus NCTC 8325.
 Staphylococcus aureus subsp. aureus NCTC 8325
 Bacteria; Firmicutes; Bacillales; Staphylococcus.
 REFERENCE 1 (bases 1 to 2456)
 Bergeon, M.C., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
 Picard, F.J. and Roy, P.H.

TITLE Highly conserved genes and their use to generate probes and primers
 JOURNAL for detection of microorganisms
 REFERENCE Patent: WO 0123604-A 1178 05-APR-2001;
 Infectio Diagnostic (I.D.I.) INC. (CA)
 FEATURES
 Source
 Location/Qualifiers
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 Db 1088 AAGAGAAAAAGATGCCAAGATATTCAA 1115
 RESULT 12
 LOCUS SSK8MECA 5596 bp DNA linear BCT 16-JAN-1998
 DEFINITION S.scituri meca gene, strain K8 (ATCC700063).
 ACCESSION Y13096
 VERSION Y13096.1 GI:2791919
 KEYWORDS meca gene; mecI gene; mecR1 gene; NTORE78; ORF142.
 SOURCE Staphylococcus scituri.
 ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus.
 REFERENCE Wu S., de Lencastre, H. and Tomasz, A.
 AUTHORS (bases 1 to 5596)
 TITLE Genetic organization of the meca region in methicillin-susceptible
 JOURNAL and methicillin-resistant strains of Staphylococcus scituri
 MEDLINE 98101461
 PUBMED 9440511
 REFERENCE 2 (bases 1 to 5596)
 Wu, S.
 TITLE Direct Submission
 JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
 AUTHORS University, 1230 York Avenue, New York NY 10021, USA
 COMMENT Related sequences X53818, X54660, L14020, X52593, Y09223.
 FEATURES
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ORIGIN
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Best local Similarity 100.0%; Pred. No. 3.7; Mismatches 0; Gaps 0;
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Db 3660 AAGCAAAAAGATGGCAAGATATTCAA 3687
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RESULT 13
SSK3MECA2
LOCUS SSK3MECA2 6368 bp DNA linear BCT 16-JAN-1998
DEFINITION S.scituri meca2 gene, strain K3 (MM2).
ACCESSION Y13095
KEYWORDS Y13095.1 GI:2791912
VERSION CTORF261 gene; meca2 gene; mecI gene; mecr1 gene; NTORF101; ORF142.
SOURCE Staphylococcus scituri.
ORGANISM Staphylococcus scituri.
REFERENCE 1 (bases 1 to 6368)
AUTHORS Wu,S., de Lencastre,H. and Tomasz,A.
TITLE Genetic organization of the meca region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus scituri
J. Bacteriol. 180 (2), 236-242 (1998)
JOURNAL 98101461
MEDLINE 9440511
PUBMED 2 (bases 1 to 6368)
REFERENCE Wu,S.
AUTHORS Direct Submission
TITLE Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences U14020, X52593, Y09223.
FEATURES
source Location/Qualifiers
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Db 4432	AAAGAAAAAAGATGGCAAAAGATATTCAA 4459				
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SAMECARLI					
LOCUS	SAMECARLI				
DEFINITION	Staphylococcus aureus meca, mecI genes and ORF142, ORF44, ORF145 and ORF224.				
ACCESSION	Y14051				
VERSION	Y14051.1				
KEYWORDS	mea gene; mecI gene; mecR1 gene; ORF142; ORF145; ORF224; ORF44; PBP2A; repressor protein; transposase.				
SOURCE	Staphylococcus aureus				
ORGANISM	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
REFERENCE	1 (bases 1 to 9047)				
AUTHORS	Wu, S.				
TITLE	Direct Submision				
JOURNAL	Submitted (27-JUN-1997) S. Wu, Laboratory of Microbiology, The Rockefeller University, 1230 York Avenue, New York, NY 10021, USA				
REFERENCE	2 (bases 1 to 9047)				
AUTHORS	Wu, S.; de Lencastre, H. and Tomasz, A.				
TITLE	Genetic organization of the meca region in methicillin-susceptible and methicillin-resistant strains of Staphylococcus sciuri				
JOURNAL	J. Bacteriol. 180 (2), 236-242 (1998)				
MEDLINE	98101461				

PUBMED FEATURES SOURCE	9440511	Location/Qualifiers 1..9047 /organism="Staphylococcus aureus" /strain="BMS-1" /db_xref="taxon:1280" complement(<1..505) /note="ORF168" /codon_start=1 /transl_table=11 /product="putative repressor" /protein_id="CAA74373.1" /db_xref="GI:2791984" /transl_table="MYNYFDGNVYKHESYDLDPBEKVSIIISIKKHIDIOEKIDTYNG LLGVSVSIHGVNNEQHVLYLPHEFEGISIAKKIKETVNPVVEANLMSALYERN FNNLSYNNLIALSIHKIGAGLIINNQLVRGANGEGEIGTLVSKVSDNVEIFHKI EDIFSOEA"
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LOCUS		Staphylococcus aureus DNA, type-IV staphylococcal cassette
DEFINITION		Chromosome mec, strain: JCS-1978(8/6-3P).
ACCESSION		AB063173
VERSION		AB063173.1 GI:17025993
KEYWORDS		
SOURCE		Staphylococcus aureus (strain: JCS-1978(8/6-3P)) DNA.
ORGANISM		Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE	1	Hiramatsu, K., Cui, L., Kuroda, M. and Ito, T. The emergence and evolution of methicillin-resistant Staphylococcus aureus Trends Microbiol. 9 (10), 486-493 (2001)
JOURNAL		21482917
MEDLINE		

REFERENCE 2
AUTHORS Ma,X.X., Ito,T., Tienasastorn,C., Jamklang,M., Chongtrakool,P.,
TITLE Boyle-Vavara,S., Damm,R.S. and Hiramatsu,K.
Novel type of Staphylococcal Cassette Chromosome mec Identified in
Community Acquired Methicillin-Resistant Staphylococcus aureus
Strains
JOURNAL Antimicrob. Agents Chemother. 46 (4), 1147-1152 (2002)
MEDLINE 21895198
REFERENCE 3 (bases 1 to 21777)
AUTHORS Xue,M.X., Ito,T., Hiramatsu,K. and Tienasastorn,C.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2001) Teryuo Ito, Juntendo University, Department
of Bacteriology, Hongo 2-1-1, Bunkyo-ku, Tokyo 113-8421, Japan
(E-mail:teruyacmed@juntendo.ac.jp, Tel:81-3-5802-1041,
Fax:81-3-5684-7830)
FEATURES
source Location/Qualifiers
1. 21777
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TGTIRATNSDNIKTVALNGYCHVILPYAKYLIINREDEVIOQMEKEDHMFESIKDEFNN
TGTIRARAVITTTSAKTIIGRLSTDIIDIANIRDTVIDYTHRTYFERSIADADIVIT
QFVAQNRKGFSDGALKMFEVNGELISIKDDHI EVAMIANVFKOMLNHOFQADVNVV
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NCTPIIINONESPTVRAVENYVIKGGYKKIADLLEDNPIYINROBYOVNITIMNNGC
GNVINOYGFEDMFPSTIVSANYEBOQRRLDKOTQOTSNDQLOKIKCPCEPNTLT
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CDS

CDS

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/transl_table=1  
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CDS
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Best local Similarity 100.0%; Pred. No. 3.3;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAGATGGCAAGATATTCAA 28
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Db 14590 AAAGAAAAGATGGCAAGATATTCAA 14617

arch completed: December 10, 2002, 20:16:59
job time : 614.209 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:03:28 ; Search time 182.547 Seconds

(Without alignments)
345.422 Million cell updates/sec

Title: US-09-865-579A-22

Sequence: 1 aaagaaaaagatgacaaagattatca 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the chance being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	28	100.0	28	24	ABR85922	Methicillin resist
2	28	100.0	39	24	ABR85928	Methicillin resist
3	28	100.0	59	20	AAK05905	Oligonucleotide pro
4	28	100.0	59	20	AAK15477	Oligonucleotide pro
5	28	100.0	89	20	AAK05906	Oligonucleotide pro
6	28	100.0	89	20	AAK15478	Probe mecA945-89
7	28	100.0	108	20	AAK15487	Probe mecA913-1020
8	28	100.0	1789	16	AAK04536	Staphylococcus aur
9	28	100.0	2007	13	AAK08599	Encodes penicillin

10	28	100.0	2007	17	AAK08568	Bacterial antibiotic
11	28	100.0	2007	19	AAK68337	Penicillin binding
12	28	100.0	2007	22	ABK76993	Staphylococcus resista
13	28	100.0	2028	24	ABK92247	Staphylococcus epi
14	28	100.0	2110	14	AAK05213	Sequence of the me
15	28	100.0	2322	13	AAK025905	HP2', Synthetic.
16	28	100.0	2455	16	AAK04538	Staphylococcus aur
17	28	100.0	2456	12	AAK01187	Staphylococcus aur
18	22.8	81.4	618	22	AAK88033	Peppermint plant o
19	21.6	77.1	47	20	AAK05908	Oligonucleotide pro
20	21.6	77.1	47	20	AAK120935	Probe mecA945-9A1
21	20.8	74.3	427	22	AAK120935	Human breast cance
22	20.8	74.3	428	22	AAK12050	Human breast cance
23	20.6	73.6	2429	22	AAK25890	Human cDNA encod
24	20.6	73.6	35832	23	ABL18126	Drosophila melanog
25	20.6	73.6	368004	24	ABL57909	Human transposite
26	20	71.4	29	20	AAK05907	Oligonucleotide pro
27	20	71.4	29	20	AAK05907	Oligonucleotide pro
28	20	71.4	29	20	AAK05909	Oligonucleotide pro
29	20	71.4	29	20	AAK05910	Oligonucleotide pro
30	20	71.4	29	20	AAK05904	Oligonucleotide pr
31	20	71.4	29	20	AAK15481	Probe mecA945-2912
32	20	71.4	29	20	AAK15482	Probe mecA945-29R
33	20	71.4	29	20	AAK15475	Probe mecA945-29D
34	20	71.4	29	20	AAK15476	Probe mecA945T for
35	20	71.4	29	20	AAK05680	Chimeric mecA945-2
36	20	71.4	29	20	AAK05681	meCA945-T target s
37	20	71.4	36	20	AAK15488	Probe mecA938-36 f
38	20	71.4	36	20	AAK15489	Human secreted pro
39	20	71.4	144	21	AAK13722	Human prostate exp
40	20	71.4	456	23	ABK07140	Human cDNA 3'-end
41	20	71.4	562	22	AAK92373	Mouse FLIP-C encod
42	20	71.4	1611	24	ABL52343	Human full-length
43	20	71.4	2037	22	AAK94091	Listeria monocytrog
44	20	71.4	2326	24	ABK070674	Kat androgen recep
45	20	71.4	2775	17	AAK47511	

ALIGNMENTS

RESULT 1
ABR85922
ID ABR85922 standard, DNA: 28 BP.
AC ABR85922;
XX 16-AUG-2002 (first entry)
DT Methicillin resistant Staphylococcus aureus detection primer #22.
DE Methicillin resistant Staphylococcus aureus; MRSA; primer; ss;
XX mecA: probe.
KW Staphylococcus aureus.
OS
XX
PN EPI160333-A2.
XX
PD 05-DEC-2001.
XX
PF 29-MAY-2001; 2001EP-0112100.
XX
PR 29-MAY-2000; 2000JP-0163149.
XX
PR 09-JUN-2000; 2000JP-0179394.
XX
PA (TOYJ) TOSOH CORP.
XX
PI Taya T, Ishiguro T, Saito J;
XX
DR WPI: 2002-395832/43.
XX
PT New oligonucleotide specific for the mecA methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related

```
PT mRNA -
XX
XX Claim 5; Page 20; 28pp; English.
XX
XX This invention relates to oligonucleotides used for cleaving, detecting
XX and amplifying the mecA gene (associated with methicillin resistance in
XX Staphylococcus aureus) or its derived RNA. The invention also comprises
XX a detection method employing an RNA amplification process, using RNA
XX derived from the mecA gene as template. Also disclosed is a detection
XX method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
XX amplification process in the presence of a complementary oligonucleotide
XX probe labelled with an intercalated fluorescent dye, where complementary
XX binding of the probe to the RNA transcription product results in a
XX change in the fluorescent property relative to that of a situation where
XX a complex formation is absent, and then measuring the fluorescence
XX intensity of the reaction solution. The oligonucleotides may be used as
XX primers or probes, for detecting methicillin-resistant S. aureus in
XX clinical samples. They may also be used therapeutically to inhibit RNA
XX reverse transcription or translation. These oligonucleotides permit
XX rapid and very sensitive detection/identification of the mecA gene, at a
XX relatively low temperature without the need for heat denaturation of
XX target RNA. The present sequence represents a methicillin resistant
XX Staphylococcus aureus (MRSA) detection oligonucleotide of the invention.
XX
SQ Sequence 28 BP; 17 A; 2 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 28; DB 24; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGGCAAGATATTCAA 28
Db 1 AAAGAAAAAGATGGCAAGATATTCAA 28

RESULT 2
ABK85928/C
ID ABK85928 standard; DNA; 39 BP.
XX
XX ABK85928:
XX
XX 16-AUG-2002 (first entry)
XX
XX Methicillin resistant Staphylococcus aureus cleavage probe #3.
XX
XX Methicillin resistant Staphylococcus Aureus; MRSA; primer; ss;
XX
XX mecA; probe.
XX
XX Staphylococcus aureus.
XX
XX
XX Key Location/Qualifiers
XX modified_base 39 /*tag= a
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XX
XX EP1160333-A2.
XX
XX 05-DEC-2001.
XX
XX 29-MAY-2001; 2001EP-0112100.
XX
XX 29-MAY-2000; 2000JP-0163149.
XX
XX 09-JUN-2000; 2000JP-0179394.
XX
XX (TOYJ ) TOSOH CORP.
XX
XX Taya T, Ishiguro T, Saito J;
XX
XX WPI; 2002-395832/43.
XX
XX New oligonucleotide specific for the mecA methicillin-resistance gene,
XX useful for cleavage, detection and amplification of the gene or related
XX mRNA
```

```
XX
XX Example 2; Page 22; 28pp; English.
XX
XX This invention relates to oligonucleotides used for cleaving, detecting
XX and amplifying the mecA gene (associated with methicillin resistance in
XX Staphylococcus aureus) or its derived RNA. The invention also comprises
XX a detection method employing an RNA amplification process, using RNA
XX derived from the mecA gene as template. Also disclosed is a detection
XX method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
XX amplification process in the presence of a complementary oligonucleotide
XX probe labelled with an intercalated fluorescent dye, where complementary
XX binding of the probe to the RNA transcription product results in a
XX change in the fluorescent property relative to that of a situation where
XX a complex formation is absent, and then measuring the fluorescence
XX intensity of the reaction solution. The oligonucleotides may be used as
XX primers or probes, for detecting methicillin-resistant S. aureus in
XX clinical samples. They may also be used therapeutically to inhibit RNA
XX reverse transcription or translation. These oligonucleotides permit
XX rapid and very sensitive detection/identification of the mecA gene, at a
XX relatively low temperature without the need for heat denaturation of
XX target RNA. The present sequence represents a methicillin resistant
XX Staphylococcus aureus (MRSA) cleaving probe used in the detection
XX method of the invention.
XX
SQ Sequence 39 BP; 5 A; 7 C; 4 G; 23 T; 0 other;

Query Match 100.0%; Score 28; DB 24; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGGCAAGATATTCAA 28
Db 33 AAAGAAAAAGATGGCAAGATATTCAA 6

RESULT 3
AAK05905
ID AAK05905 standard; RNA; 59 BP.
XX
XX AAK05905:
XX
XX 07-MAY-1999 (first entry)
XX
XX Oligonucleotide probe meca932-59R.
XX
XX Hybridization; RNase H; scissile linkage; nucleic acid detection;
XX
XX gene detection; polyamine; probe; ss.
XX
XX Synthetic.
XX
XX WO9901570-A2.
XX
XX 14-JAN-1999.
XX
XX 03-JUL-1998; 98WO-CA00631.
XX
XX 22-JUN-1998; 98US-0090273.
XX
XX 03-JUL-1997; 97US-0051827.
XX
XX 18-MAY-1998; 98US-0086021.
XX
XX (IDBI-) ID BIOMEDICAL CORP.
XX
XX Bryan RN, Cloney LP, Farnworth BA, Marostemaki AJ;
XX
XX WPI; 1999-106070/09.
XX
XX Increasing the hybridization rate between two nucleic acids - using
XX ribonuclease H (RNase H) and/or a polyamine, useful for detecting
XX nucleic acids of interest in a sample
XX
XX Example 1; Page 15; 45pp; English.
XX
XX The invention relates to methods of increasing the hybridization rate
```

CC between two nucleic acids. One method comprises construction of two
CC nucleic acids and a polyamine, and hybridizing both nucleic acids
CC together, under suitable conditions. Also provided is a similar method
CC involving two nucleic acids with RNase H, where both nucleic acids do
CC not contain a scissile linkage, and if one nucleic acid is DNA, then the
CC other is RNA. The methods are useful for (in)directly detecting nucleic
CC acids of interest in a sample. They may be applied to short and long
CC nucleic acids. The acceleration of rate reactions in gene detection
CC assays, using RNase H and/or polyamines (under conditions of low salt
CC concentration), produces a lower background and, therefore, a greater
CC signal to noise ratio. Sequences AAX05903-914 represent oligonucleotide
CC probes used in the course of the invention.

XX
SQ Sequence 59 BP; 30 A; 8 C; 9 G; 12 U; 0 other;

Query Match 100.0%; Score 28; DB 20; Length 59;
Best Local Similarity 85.7%; Pred. No. 0.23;
Matches 24; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Y 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
|||||
JB 22 AAAGAAAAAGATGCGCAAGATATTCAA 49

RESULT 4
AAX15477
ID AAX15477 standard; RNA; 59 BP.

XX AAX15477;

XX 07-MAY-1999 (first entry)

DE Probe mecA932-59R for detecting an antibiotic resistant mecA gene.

XX
KM Antibiotic resistant mecA gene; transmission; treatment;
KM methicillin resistant; Staphylococcus; probe; ss.

XX
OS Synthetic.
XX Staphylococcus sp.

PN WO9901572-A2.

XX
PD 14-JAN-1999.

XX
PV 03-JUL-1998; 98WO-CA00633.

XX
PR 22-JUN-1998; 98US-0090276.

PR 03-JUL-1997; 97US-0051643.

XX
R 18-MAY-1998; 98US-0086020.

XX
PA (IDBI-) ID BIOMEDICAL CORP.

XX
PI Bekkaoui F, Cloney LP;

XX
DR WPI; 1999-106072/09.

XX
PT Method for determining the presence of an antibiotic resistant mecA
PT gene in a sample - using a scissile link containing nucleic acid
PT probe for antibiotic resistant mecA gene

XX
PS Example 1; Page 16; 59pp; English.

XX
CC The present sequence represents a probe used for determining the
CC presence of an antibiotic resistant mecA gene in a biological sample.
CC The method provides a means for the rapid detection, for both
CC the prevention of transmission and treatment of, methicillin resistant
CC Staphylococcus species.

XX
SQ Sequence 59 BP; 30 A; 8 C; 9 G; 12 U; 0 other;

Query Match 100.0%; Score 28; DB 20; Length 59;
Best Local Similarity 85.7%; Pred. No. 0.23;
Matches 24; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
|||||
DB 22 AAAGAAAAAGATGCGCAAGATATTCAA 49

RESULT 5
AAX05906/C
ID AAX05906 standard; DNA; 89 BP.

XX AAX05906;

XX 07-MAY-1999 (first entry)

DE Oligonucleotide probe ccmecA915-89.

XX
KM Hybridization; RNase H; scissile linkage; nucleic acid detection;
KM gene detection; polyamine; probe; ss.

XX
OS Synthetic.

PN WO9901570-A2.

XX
PD 14-JAN-1999.

XX
PE 03-JUL-1998; 98WO-CA00631.

XX
PR 22-JUN-1998; 98US-0090273.

PR 03-JUL-1997; 97US-0051827.

XX
PR 18-MAY-1998; 98US-0086021.

XX
PA (IDBI-) ID BIOMEDICAL CORP.

XX
PI Bryan RN, Cloney LP, Farnworth BA, Marostemaki AJ;

XX
DR WPI; 1999-106070/09.

XX
PT Increasing the hybridization rate between two nucleic acids - using
PT ribonuclease H (RNase H) and/or a polyamine, useful for detecting
PT nucleic acids of interest in a sample

XX
PS Example 1; Page 15; 45pp; English.

XX
CC The invention relates to methods of increasing the hybridization rate
CC between two nucleic acids. One method comprises construction of two
CC nucleic acids and a polyamine, and hybridizing both nucleic acids
CC together, under suitable conditions. Also provided is a similar method
CC involving two nucleic acids with RNase H, where both nucleic acids do
CC not contain a scissile linkage, and if one nucleic acid is DNA, then the
CC other is RNA. The methods are useful for (in)directly detecting nucleic
CC acids of interest in a sample. They may be applied to short and long
CC nucleic acids. The acceleration of rate reactions in gene detection
CC assays, using RNase H and/or polyamines (under conditions of low salt
CC concentration), produces a lower background and, therefore, a greater
CC signal to noise ratio. Sequences AAX05903-914 represent oligonucleotide
CC probes used in the course of the invention.

XX
SQ Sequence 89 BP; 20 A; 13 C; 13 G; 43 T; 0 other;

Query Match 100.0%; Score 28; DB 20; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
|||||
DB 50 AAAGAAAAAGATGCGCAAGATATTCAA 23

RESULT 6
AAX15478/C
ID AAX15478 standard; DNA; 89 BP.
XX
AC AAX15478;

```

XX 07-MAY-1999 (first entry)
DE Probe cmeCA945-89 for detecting an antibiotic resistant mecA gene.
XX
XX Antibiotic resistant mecA gene; transmission; treatment:
KM methicillin resistant; Staphylococcus; probe; ss.
OS
OS Synthetic.
OS Staphylococcus sp.
XX
XX WO9901572-A2.
XX
XX 14-JAN-1999.
XX
XX 03-JUL-1998; 98WO-CA00633.
XX
XX 22-JUN-1998; 98US-0090276.
XX
XX 03-JUL-1997; 97US-0051643.
XX
XX 18-MAY-1998; 98US-0086020.
XX
XX (IDBI-) ID BIOMEDICAL CORP.
XX
XX Bekkaoui F, Cloney LP;
XX
XX WPI; 1999-106072/09.
XX
XX Method for determining the presence of an antibiotic resistant mecA
XX PT gene in a sample - using a scissile link containing nucleic acid
XX PT probe for antibiotic resistant mecA gene
XX
XX
XX Claim 5; Page 16; 59pp; English.
XX
XX The present sequence represents a probe used for determining the
XX CC presence of an antibiotic resistant mecA gene in a biological sample.
XX CC The method provides a means for the rapid detection, for both
XX CC the prevention of transmission and treatment of, methicillin resistant
XX CC Staphylococcus species.
XX
XX Sequence 89 BP; 20 A; 13 C; 13 G; 43 T; 0 other;
SQ
Query Match 100.0%; Score 28; DB 20; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAAGAAAAAGATGCCAAGATATTCAA 28
DB 50 AAAGAAAAAGATGCCAAGATATTCAA 23

```

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PR 03-JUL-1997; 97US-0051643.
PR 18-MAY-1998; 98US-0086020.
XX
XX (IDBI-) ID BIOMEDICAL CORP.
XX
XX Bekkaoui F, Cloney LP;
XX
XX WPI; 1999-106072/09.
XX
XX Method for determining the presence of an antibiotic resistant mecA
XX PT gene in a sample - using a scissile link containing nucleic acid
XX PT probe for antibiotic resistant mecA gene
XX
XX
XX Claim 4; Page 17; 59pp; English.
XX
XX The present sequence represents a probe used for determining the
XX CC presence of an antibiotic resistant mecA gene in a biological sample.
XX CC The method provides a means for the rapid detection, for both
XX CC the prevention of transmission and treatment of, methicillin resistant
XX CC Staphylococcus species.
XX
XX Sequence 108 BP; 53 A; 14 C; 16 G; 25 T; 0 other;
SQ
Query Match 100.0%; Score 28; DB 20; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAAGAAAAAGATGCCAAGATATTCAA 28
DB 42 AAAGAAAAAGATGCCAAGATATTCAA 69

```

RESULT 8

```

AAT04536
ID AAT04536 standard; cDNA to mRNA; 1789 BP.
XX
XX AAT04536;
XX
XX 11-APR-1996 (first entry)
XX
XX Staphylococcus aureus 'mecA protein coding sequence.
XX DE
XX methicillin-resistant Staphylococcus aureus; MRSA; 'mecA protein;
XX KM antibiotic resistance; ds.
XX
XX Staphylococcus aureus.
XX OS
XX Key Location/Qualifiers
XX FT 1..1608
XX FT /tag= a
XX CDS /product= 'mec_A_protein

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JP07209294-A.

```

XX
XX 11-AUG-1995.
XX
XX 10-JAN-1994; 94JP-0012226.
XX
XX 10-JAN-1994; 94JP-0012226.
XX
XX 10-JAN-1994; 94JP-0012226.
XX
XX (DENK-) DENKA SEIKEN KK.
XX PA (KANNA/) KANANO M.
XX PA (MITU ) MITSUBISHI CHEM CORP.
XX
XX WPI; 1995-313917/41.
XX DR P-PSDB; AAR80035.
XX
XX New 'mec A protein and DNA encoding it - used for the detection of
XX PT methicillin-resistant Staphylococcus aureus
XX
XX Claim 5; Page 11-13; 15pp; Japanese.
XX
XX The present sequence codes for the 'mec A protein which controls

```

CC methicillin resistance in methicillin-resistant Staph. aureus. The
 CC 'mec A' protein (mol. wt. 40000) is useful for preparation of
 CC an antiserum specific for MRSA, thereby allowing methicillin-resistant
 CC and methicillin-sensitive strains to be distinguished. The coding
 CC sequence was obtained by PCR amplification of the mec A sequence
 CC (see AAT04538) using primers AAT04537 and AAT04539.
 CC N.B. In the sequence listing of the patent specification, the
 CC sequence length is stated to be 1785 bp.
 CC
 SQ Sequence 1789 BP; 735 A; 263 C; 302 G; 489 T; 0 other;
 Query Match 100.0%; Score 28; DB 16; Length 1789;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGCAAAAAGATGCCAAGATATTCAA 28
 Db 549 AAGCAAAAAGATGCCAAGATATTCAA 576
 RESULT 9
 ID AAT28599 standard; DNA; 2007 BP.
 AC AAT28599;
 XX
 XX 19-FEB-1993 (first entry)
 DF Encodes penicillin binding protein PBP2A-27R.
 XX
 XX Penicillin; antibiotic; bacteria; methicillin; staphylococci;
 KW soluble; chelating peptide; MRS infection; methicillin resistant;
 KW strain.
 XX
 OS Staphylococcus aureus strain 27R.
 XX
 FU Key Location/Qualifiers
 FT CDS 1..2007
 FT /tag= a
 XX
 XX EP505151-A.
 PN 23-SEP-1992.
 PD
 XX
 PF 18-MAR-1992; 92EP-0302298.
 XX
 PR 19-MAR-1991; 91US-0672704.
 XX
 XX (ELIL) LILLY & CO ELI.
 XX
 PI Blaszczak IC, Skatrud PL, Smith MC, Wu CYE;
 XX
 DR WPI; 1992-318034/39.
 XX
 XX Polynucleotide cpd. encoding PBP 2A-27R protein or its deriv. -
 PT contains PBP isolated from staphylococcus aureus and is used to
 PT treat methicillin resistant staphylococci
 XX
 XX Disclosure; Page 14; 101pp; English.
 PS
 XX This sequence encodes a PBP2A penicillin binding protein isolated
 CC from S. aureus strain 27R. A cDNA library was constructed from
 CC S. aureus DNA in lambda phage EMBL3. Packaging extracts from this
 CC then used to infect E. coli CJ236. Plaques were screened for the
 CC presence of the mecA-27R gene by a probe produced by PCR amplification
 CC of the mecA gene using primers Q28600.1. Positive plaques were purified
 CC and digested with HindIII, and this fragment digested with XbaI and
 CC cloned into M13amp18 and M13amp19 for sequencing.
 CC
 SQ Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
 Query Match 100.0%; Score 28; DB 13; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 0.34;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAGCAAAAAGATGCCAAGATATTCAA 28
 Db 948 AAGCAAAAAGATGCCAAGATATTCAA 975
 RESULT 10
 ID AAT28568 standard; DNA; 2007 BP.
 AC AAT28568;
 XX
 XX 01-APR-1997 (first entry)
 DT
 XX
 DE Bacterial antibiotic resistance gene, mecA, probe.
 KW
 KW Detection; probe; amplification primer; bacterial pathogen; pneumonia;
 KW Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
 KW Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
 KW Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
 KW Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
 KW Haemophilus influenzae; Moraxella catarrhalis; septicaemia; meningitis;
 KW infection; intra-abdominal infection; skin infection;
 KW bacterial resistance; beta-lactam antibiotic; ds.
 XX
 OS Synthetic.
 XX
 PN WO9608582-A2.
 PD
 XX 21-MAR-1996.
 PP
 XX 12-SEP-1995; 95WO-CA00528.
 XX
 PR 12-SEP-1995. 94US-0304732.
 XX
 PA (BERG) BERGERON M. G.
 PA (OUEL) OUELLETTE M.
 PA (ROY P H.) ROY P H.
 XX
 PI Bergeron MC, Ouellette M, Roy PH;
 XX
 DR WPI; 1996-179953/18.
 XX
 XX Method for the detection of bacterial species using probes and
 PT primers - allows detection and quantification of antibiotic
 PT resistant bacteria in patients, the environment and food
 XX
 PS Claim 91: Page 144-145; 216pp; English.
 XX
 CC The sequences given in AAT28560-76 represent fragments derived from
 CC bacterial antibiotic resistance genes which were used as probes in the
 CC method of the invention for the detection of bacterial species in a
 CC sample. The method of the invention comprises using probes and/or
 CC amplification primers which are specific, ubiquitous and sensitive for
 CC determining the presence and/or amount of nucleic acids from selected
 CC bacterial species in any sample, where the bacterial nucleic acid
 CC comprises a selected target region hybridisable with the probes or
 CC primers. The method comprises contacting the sample with the probes
 CC or primers and detecting the presence and/or amount of hybridised
 CC primers or amplification products as and indication of the presence
 CC and/or amount of the bacterial species. This method may be used to
 CC detect commonly encountered bacterial pathogens, e.g. Escherichia coli,
 CC Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis,
 CC Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus
 CC epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus,
 CC Streptococcus pyogenes, Haemophilus influenzae and Moraxella
 CC catarrhalis. These bacterial species are associated with approx. 90% of
 CC urinary tract infections and with a high percentage of other severe
 CC infections including septicaemia, meningitis, pneumonia, intra-abdominal
 CC infections, skin infections and other severe respiratory tract
 CC infections. The method may also be used to evaluate a bacterial
 CC resistance to beta-lactam antibiotics.

XX Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
SQ
Query Match 100.0%; Score 28; DB 17; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGCAAAAAGATGCCAAGATATTCAA 28
AAAAAAAAAAAAAAAAAAAAAAAAAAAA
DB 948 AAGCAAAAAGATGCCAAGATATTCAA 975
RESULT 11
AAV68337
ID AAV68337 standard; DNA; 2007 BP.
XX
XX AAV68337;
AC
XX
XX 21-JUN-1999 (first entry)
DT
XX
XX Penicillin binding protein PBP2A meca-27R gene of *S. aureus* 27R.
X
X Penicillin binding protein; PBP2A-27A; meca-27R gene;
X methicillin resistance; antibiotic; assay; purification; ss.
X
X Staphylococcus aureus.
X
X EP875578-A2.
X
X 04-NOV-1998.
X
X 18-MAR-1992; 92EP-0302298.
X
X 19-MAR-1991; 91US-0672704.
X
X (ELIL) LILLY & CO ELI.
X
X Blaszcak LC, Skatrud PL, Smith MC, Wu CE;
X
X WPI: 1998-559443/48.
X P-PSDB: AAM81149.
X
X New Staphylococcus aureus soluble penicillin-binding proteins and
X their derivatives - useful for screening for compounds effective
X against methicillin resistant organisms
XX
XX
PS Disclosure: Page 14-16; 97pp; English.
XX
XX This meca-27R gene encodes penicillin binding protein 2A (PBP2A-27R)
X responsible for the methicillin resistance of Staphylococcus aureus
X strain 27R. The invention provides new PBPs of formula SP-L-PBP2As,
X where: SP is 0 or a signal peptide (preferably from the ampC, ompA or
X Met-Gly-CP-(Pro)n-PBP2As, where CP = 0 or a chelating peptide (see
X AAM81151-58) of formula (His)x-(A)y (His)z and A-an amino acid,
X x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above
X polypeptide where each monomer unit is the same or different; Pro
X is proline, n = 0 or 1; and PBP2As is soluble PBP2A-27R protein (see
X AAM81159-62). Also claimed are polynucleotides encoding specific
X soluble PBP2A compounds. The new PBP2A-27R proteins are useful for
X assaying for agents useful as antibiotics against methicillin
X resistant Staphylococcus strains by creating a kinetically inert
X complex between a support-immobilised transition ion and a modified
X soluble PBP2A protein comprising a chelating agent, which screens
X for agents which bind to PBP2A proteins (disclosed). Soluble forms
X of PBP2A-27R protein facilitate crystallisation as they lack their
X transmembrane association region, and so are useful for x-ray
X crystallography studies of the protein, assisting in the design of
X antibiotic compounds against methicillin resistant Staphylococcus
X strains (disclosed). The chelating peptide operably linked to the
X BPA-27R proteins is useful for purifying PBPs.
XX
SQ Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;

Query Match 100.0%; Score 28; DB 19; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGCAAAAAGATGCCAAGATATTCAA 28
AAAAAAAAAAAAAAAAAAAAAAAAAAAA
DB 948 AAGCAAAAAGATGCCAAGATATTCAA 975
RESULT 12
ABA76993
ID ABA76993 standard; DNA; 2007 BP.
XX
XX ABA76993;
AC
XX
XX 28-JAN-2002 (first entry)
DT
XX
XX Antibiotic resistance detection polynucleotide SEQ ID NO 169.
X
X Detection; bacterial species; animal; food; environment;
X antibiotic resistance; ds.
X
X Unidentified.
X
X NZ501596-A.
X
X 29-JUN-2001.
X
X 12-SEP-1995; 95NZ-0501596.
X
X 12-SEP-1995; 95NZ-0501596.
X
X (IDI1-) IDI INFECTIO DIAGNOSTIC INC.
X
X Bergeron MC, Ouellette M, Roy PH;
X
X WPI: 2001-613034/71.
X
X Method for detecting target bacterial species in a sample, comprises
X detecting the presence or amount of bacterial nucleic acid amplified by
X a primer derived from bacterial DNA, specific for the target bacterial
X species -
XX
XX Claim 16; Page 159-160; 168pp; English.
XX
XX The invention relates to detecting target bacterial species suspected to
X be present in a sample, comprising contacting nucleic acids of target
X bacterial species with an amplification primer pair derived from a
X bacterial DNA fragment (ABA76825-ABA76861) specific for the target
X bacterial species but ubiquitous for different strains, amplifying the
X nucleic acid and detecting the presence or amount of an amplified
X sequence as an indication of the presence or amount of the target
X bacterial species. The invention includes primers and probes
X (ABA76862-ABA76984) against the target bacterial species, especially
X *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *P. mirabilis*, *S. pneumoniae*,
X *S. aureus*, *S. epidermidis*, *E. faecalis*, *S. saprophyticus*, *S. pyogenes*,
X *H. influenzae*, *M. catarrhalis* and/or group A Streptococci producing
X exotoxin A gene spe A, suspected to be present in a sample which is
X obtained from human patients, animals, environment or food, and which
X consists of one or more bacterial colonies. Oligonucleotide
X probes and primers complementary to the bacterial genes encoding
X resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aadB,
X aacC1, aacC2, aacC3, aacA4, meca, vanA, vanH, vanX, satA, aacA-apd, vat,
X vga, msrA, sul and/or int (ABA76985-ABA77001) are also useful to identify
X commonly encountered and clinically important resistance genes. The
X invention provides a rapid method of bacterial identification that can be
X achieved, which reduces the time currently required for the
X identification of pathogens in the clinical laboratory.
XX
SQ Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
Query Match 100.0%; Score 28; DB 22; Length 2007;


```

PD 17-JUN-1992.
XX
XX 31-OCT-1990; 90JP-0296708.
XX
XX 31-OCT-1990; 90JP-0296708.
XX
XX (SHIO ) SHIONOGI & CO LTD.
XX
XX WPI; 1992-253403/31.
XX
XX Detection of PBP2' gene for determ. of methicillin-resistance -
XX usefu esp. for detection of methicillin-resistance
XX staphylococcus aureus
XX
XX Disclosure; Fig 1; 9pp; Japanese.
XX
XX The sequence given is the PBP2' gene. This gene could be detected
XX by the primer sequences given in AA025897-904. Due to the results of
XX this amplification reaction resistance to methicillin in Staphylococcus
XX aureus could be determined.
XX
XX Sequence 2322 BP; 940 A; 324 C; 389 G; 669 T; 0 other;
XX
XX Query Match
XX Best Local Similarity 100.0%; Score 28; DB 13; Length 2322;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
XX ||||||||||||||||||||||||||||
XX Db 954 AAAGAAAAAGATGCGCAAGATATTCAA 981

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Job time : 184.547 secs

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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:03:28 : Search time 130.391 Seconds
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Title: US-09-865-579A-21
Perfect score: 20
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Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	24	ABK85911
2	20	100.0	20	24	ABK85921
3	20	100.0	39	24	ABK85928
4	20	100.0	59	20	AAK05905
5	20	100.0	59	20	AAK15477
6	20	100.0	89	20	AAK05906
7	20	100.0	89	20	AAK15478
8	20	100.0	108	20	AAK15487
9	20	100.0	1789	16	AAK04536

C 10	20	100.0	2007	13	AAQ28599	Encodes penicillin
C 11	20	100.0	2007	17	AAK28568	Bacterial antibiot
C 12	20	100.0	2007	19	AAV68337	Penicillin binding
C 13	20	100.0	2007	22	ABA76993	Antibiotic resista
C 14	20	100.0	2028	24	ABN92247	Staphylococcus epi
C 15	20	100.0	2110	14	AA035213	Sequence of the me
C 16	20	100.0	2322	13	AA025905	ppg2', synthelec.
C 17	20	100.0	2455	16	AAK04538	Staphylococcus aur
C 18	20	100.0	2456	22	AAH01187	Staphylococcus aur
C 19	17.4	87.0	369	24	ABO85506	Arabidopsis thalia
C 20	17.4	87.0	2961	21	AC48316	Arabidopsis thalia
C 21	16.8	84.0	350	24	ABQ85831	Arabidopsis thalia
C 22	16.8	84.0	16484	20	AAK13095	Enterococcus faeca
C 23	16.4	82.0	2052	23	ABL07785	Drosophila melanog
C 24	16.4	82.0	4437	23	ABL07784	Drosophila melanog
C 25	16	80.0	199	21	AAK10590	Fusarium venenatum
C 26	15.8	79.0	696	21	AAAA4046	Human secreted exp
C 27	15.8	79.0	1187	24	ABQ38096	Oligonucleotide to
C 28	15.8	79.0	1187	24	ABQ38097	Oligonucleotide to
C 29	15.8	79.0	1598	23	ABL21005	Drosophila melanog
C 30	15.8	79.0	1722	23	ABL29687	Drosophila melanog
C 31	15.8	79.0	3423	23	ABL24346	Drosophila melanog
C 32	15.8	79.0	3829	23	ABL21004	Drosophila melanog
C 33	15.8	79.0	4010	23	ABL29686	Drosophila melanog
C 34	15.8	79.0	8738	23	ABL11376	Drosophila melanog
C 35	15.8	79.0	9151	22	ABA14677	Human nervous syst
C 36	15.8	79.0	9153	22	ABA14676	Human nervous syst
C 37	15.8	79.0	19866	22	AAK37522	Human musculoskele
C 38	15.8	79.0	160271	22	AAK85750	Hipolar affective
C 39	15.8	79.0	160271	22	AAK85756	Human chromosome 1
C 40	15.8	79.0	160271	22	AAK85758	Human chromosome 1
C 41	15.8	79.0	160271	22	AAK85759	Human chromosome 1
C 42	15.8	79.0	160271	22	AAK85760	Human chromosome 1
C 43	15.8	79.0	160271	22	AAK85761	Human chromosome 1
C 44	15.8	79.0	160271	22	AAK85762	Human chromosome 1
C 45	15.8	79.0	160271	22	AAK85763	Human chromosome 1

ALIGNMENTS

RESULT 1	ABK85911	standard; DNA: 20 BP.
ID	ABK85911	
AC	ABK85911	
DT	16-AUG-2002	(first entry)
DE	Methicillin resistant Staphylococcus aureus detection primer #1.	
XX	Methicillin resistant Staphylococcus aureus; MRSA; primer: SS;	
KW	mechA; Probe.	
OS	Staphylococcus aureus.	
XX	EP1160333-A2.	
PN	05-DEC-2001.	
PD	29-MAY-2001; 2001BP-0112100.	
PF	29-MAY-2000; 2000JP-0163149.	
PR	09-JUN-2000; 2000JP-0179394.	
XX	(TORI) TOSOH CORP.	
XX	Taya T, Ishiguro T, Saito J;	
PI	WPI; 2002-395832/43.	
DR	New oligonucleotide specific for the mechA methicillin-resistance gene,	
XX	useful for cleavage, detection and amplification of the gene or related	
PT		

PT mRNA -
XX Claim 1; Page 16; 28pp; English.
XX
CC This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the mecA gene (associated with methicillin resistance in
CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the mecA gene as template. Also disclosed is a detection
CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant *S. aureus* in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the mecA gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 3 C; 4 G; 9 T; 0 other;
Query Match 100.0%; Score 20; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTAGTGAATATCTTGGC 20
Db 1 GTTAGTGAATATCTTGGC 20
RESULT 2
ABK85921
ID ABK85921 standard; DNA: 20 BP.
XX
AC ABK85921;
XX
DT 16-AUG-2002 (first entry)
XX
DE Methicillin resistant *Staphylococcus aureus* detection primer #21.
XX
KW Methicillin resistant *Staphylococcus Aureus*; MRSA; primer; ss;
XX
XX mecA; probe.
XX
XX *Staphylococcus aureus*.
XX
N EP1160333-A2.
XX
PD 05-DEC-2001.
XX
PF 29-MAY-2001; 2001EP-0112100.
XX
PR 29-MAY-2000; 2000JP-0163149.
PR 09-JUN-2000; 2000JP-0179394.
XX
PA (TOYJ) TOSOH CORP.
XX
PI Taya T, Ishiguro T, Salto J;
XX
DR WPI: 2002-395832/43.
XX
XX New oligonucleotide specific for the mecA methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related
PT mRNA -
XX
XX Claim 5; Page 19; 28pp; English.
XX
CC This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the mecA gene (associated with methicillin resistance in

CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the mecA gene as template. Also disclosed is a detection
CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant *S. aureus* in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the mecA gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC *Staphylococcus aureus* (MRSA) detection oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 3 C; 4 G; 9 T; 0 other;
Query Match 100.0%; Score 20; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTAGTGAATATCTTGGC 20
Db 1 GTTAGTGAATATCTTGGC 20
RESULT 3
ABK85928
ID ABK85928 standard; DNA: 39 BP.
XX
AC ABK85928;
XX
DT 16-AUG-2002 (first entry)
XX
DE Methicillin resistant *Staphylococcus aureus* cleavage probe #3.
XX
KW Methicillin resistant *Staphylococcus Aureus*; MRSA; primer; ss;
XX
XX mecA; probe.
XX
XX *Staphylococcus aureus*.
XX
OS
XX
FH Key Location/Qualifiers
FH modified_base 39
FT /*tag= a
FT /*note= "Amidated"
XX
PN EP1160333-A2.
XX
PD 05-DEC-2001.
XX
PF 29-MAY-2001; 2001EP-0112100.
XX
PR 29-MAY-2000; 2000JP-0163149.
PR 09-JUN-2000; 2000JP-0179394.
XX
PA (TOYJ) TOSOH CORP.
XX
PI Taya T, Ishiguro T, Salto J;
XX
DR WPI: 2002-395832/43.
XX
XX New oligonucleotide specific for the mecA methicillin-resistance gene,
PT useful for cleavage, detection and amplification of the gene or related
PT mRNA -
XX
XX Example 2; Page 22; 28pp; English.
XX
XX This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the mecA gene (associated with methicillin resistance in
CC *Staphylococcus aureus*) or its derived RNA. The invention also comprises

CC a detection method employing an RNA amplification process, using RNA
CC derived from the meca gene as template. Also disclosed is a detection
CC method for a methicillin-resistant *S. aureus* (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant *S. aureus* in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the meca gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC *Staphylococcus aureus* (MRSA) cleaving probe used in the detection
CC method of the invention.

XX Sequence 39 BP; 5 A; 7 C; 4 G; 23 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.5; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 0;

OY 1 GTTAGTGAATATCTTTGCC 20
|||||
Db 1 GTTAGTGAATATCTTTGCC 20

RESULT 4
AA05905/c
ID AA05905 standard; RNA; 59 BP.

XX AAX05905;

DT 07-MAY-1999 (first entry)

XX Oligonucleotide probe meca932-59R.

XX Hybridization; RNase H; scissile linkage; nucleic acid detection;

KW gene detection; polyamine; probe; ss.

XX Synthetic.

XX MO9901570-A2.

PD 14-JAN-1999.

XX 03-JUL-1998; 98WO-CA00631.

FR 22-JUN-1998; 98US-0090273.

PR 03-JUL-1997; 97US-0051827.

PR 18-MAY-1998; 98US-0086021.

XX (IDBI-) ID BIOMEDICAL CORP.

PI Bryan RN, Cloney LP, Farnworth BA, Marostemaki AJ;

DR WPI: 1999-106070/09.

PT Increasing the hybridization rate between two nucleic acids - using
PP ribonuclease H (RNase H) and/or a polyamine, useful for detecting
XX nucleic acids of interest in a sample

XX Example 1; Page 15; 45pp; English.

XX The invention relates to methods of increasing the hybridization rate
CC between two nucleic acids. One method comprises construction of two
CC nucleic acids and a polyamine, and hybridizing both nucleic acids
CC together, under suitable conditions. Also provided is a similar method
CC involving two nucleic acids with RNase H, where both nucleic acids do
CC not contain a scissile linkage, and if one nucleic acid is DNA, then the
CC other is RNA. The methods are useful for (in)directly detecting nucleic

CC acids of interest in a sample. They may be applied to short and long
CC nucleic acids. The acceleration of rate reactions in gene detection
CC assays, using RNase H and/or polyamines (under conditions of low salt
CC concentration), produces a lower background and, therefore, a greater
CC signal to noise ratio. Sequences AAX05903-914 represent oligonucleotide
CC probes used in the course of the invention.

XX Sequence 59 BP; 30 A; 8 C; 9 G; 12 U; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 0;

OY 1 GTTAGTGAATATCTTTGCC 20
|||||
Db 54 GTTAGTGAATATCTTTGCC 35

RESULT 5
AAX15477/c
ID AAX15477 standard; RNA; 59 BP.

XX AAX15477;

DT 07-MAY-1999 (first entry)

XX Probe meca932-59R for detecting an antibiotic resistant meca gene.

XX Antibiotic resistant meca gene; transmission; treatment;

KW methicillin resistant; *Staphylococcus*; probe; ss.

XX Synthetic.

XX *Staphylococcus* sp.

XX MO9901572-A2.

PD 14-JAN-1999.

XX 03-JUL-1998; 98WO-CA00633.

FR 22-JUN-1998; 98US-0090276.

PR 03-JUL-1997; 97US-0051643.

PR 18-MAY-1998; 98US-0086020.

XX (IDBI-) ID BIOMEDICAL CORP.

PI Bekkaoui F, Cloney LP;

DR WPI: 1999-106072/09.

PT Method for determining the presence of an antibiotic resistant meca
PP gene in a sample - using a scissile link containing nucleic acid
XX probe for antibiotic resistant meca gene

XX Example 1; Page 16; 59pp; English.

XX The present sequence represents a probe used for determining the
CC presence of an antibiotic resistant meca gene in a biological sample.
CC The method provides a means for the rapid detection, for both
CC the prevention of transmission and treatment of, methicillin resistant
CC *Staphylococcus* species.

XX Sequence 59 BP; 30 A; 8 C; 9 G; 12 U; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 0;

OY 1 GTTAGTGAATATCTTTGCC 20
|||||
Db 54 GTTAGTGAATATCTTTGCC 35

```

RESULT 6
AA05906
ID AAX05906 standard; DNA: 89 BP.
XX
AC AAX05906;
XX
DT 07-MAY-1999 (first entry)
XX
DE Oligonucleotide probe cmeCA915-89.
XX
KW Hybridization; RNase H; scissile linkage; nucleic acid detection;
XX gene detection; polyamine; probe; ss.
XX
OS Synthetic.
XX
PN MO9901570-A2.
XX
PD 14-JAN-1999.
XX
PF 03-JUL-1998; 98WO-CA00631.
XX
PR 22-JUN-1998; 98US-0090273.
XX 03-JUL-1997; 97US-0051827.
XX 18-MAY-1998; 98US-0086021.
XX
PA (IDBI-) ID BIOMEDICAL CORP.
XX
PI Bryan RN, Cloney LP, Farnworth BA, Marostemaki AJ;
XX
DR WPI: 1999-106070/09.
XX
PT Increasing the hybridization rate between two nucleic acids - using
XX ribonuclease H (RNase H) and/or a polyamine, useful for detecting
XX nucleic acids of interest in a sample
XX
PS Example 1; Page 15; 45pp; English.
XX
CC The invention relates to methods of increasing the hybridization rate
XX between two nucleic acids. One method comprises construction of two
XX nucleic acids and a polyamine, and hybridizing both nucleic acids
XX together, under suitable conditions. Also provided is a similar method
XX involving two nucleic acids with RNase H, where both nucleic acids do
XX not contain a scissile linkage, and if one nucleic acid is DNA, then the
XX other is RNA. The methods are useful for (in)directly detecting nucleic
XX acids of interest in a sample. They may be applied to short and long
XX assays, using RNase H and/or polyamines (under conditions of low salt
XX concentration), produces a lower background and, therefore, a greater
XX signal to noise ratio. Sequences AAX05903-914 represent oligonucleotide
XX probes used in the course of the invention.
XX
SQ Sequence 89 BP; 20 A; 13 C; 13 G; 43 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTACTGAAATATCTTGGC 20
   |||||||
DB 18 GTTACTGAAATATCTTGGC 37

RESULT 7
AAX15478
ID AAX15478 standard; DNA: 89 BP.
XX
AC AAX15478;
XX
DT 07-MAY-1999 (first entry)
XX
DE Probe cmeCA945-89 for detecting an antibiotic resistant meca gene.
XX
KW Antibiotic resistant meca gene; transmission; treatment;

```

```

KW methicillin resistant; Staphylococcus; probe; ss.
XX
OS Synthetic.
XX
OS Staphylococcus sp.
XX
PN MO9901572-A2.
XX
PD 14-JAN-1999.
XX
PF 03-JUL-1998; 98WO-CA00633.
XX
PR 22-JUN-1998; 98US-0090276.
XX 03-JUL-1997; 97US-0051643.
XX 18-MAY-1998; 98US-0086020.
XX
PA (IDBI-) ID BIOMEDICAL CORP.
XX
PI Bekkaoui F, Cloney LP;
XX
DR WPI: 1999-106072/09.
XX
PT Method for determining the presence of an antibiotic resistant meca
XX gene in a sample - using a scissile link containing nucleic acid
XX probe for antibiotic resistant meca gene
XX
PS Claim 5; Page 16; 59pp; English.
XX
CC The present sequence represents a probe used for determining the
XX presence of an antibiotic resistant meca gene in a biological sample.
XX The method provides a means for the rapid detection, for both
XX the prevention of transmission and treatment of, methicillin resistant
XX Staphylococcus species.
XX
SQ Sequence 89 BP; 20 A; 13 C; 13 G; 43 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTACTGAAATATCTTGGC 20
   |||||||
DB 18 GTTACTGAAATATCTTGGC 37

RESULT 8
AAX15487/C
ID AAX15487 standard; DNA: 108 BP.
XX
AC AAX15487;
XX
DT 07-MAY-1999 (first entry)
XX
DE Probe meCA913-1020 for detecting an antibiotic resistant meca gene.
XX
KW Antibiotic resistant meca gene; transmission; treatment;
XX methicillin resistant; Staphylococcus; probe; ss.
XX
OS Synthetic.
XX
OS Staphylococcus sp.
XX
PN MO9901572-A2.
XX
PD 14-JAN-1999.
XX
PF 03-JUL-1998; 98WO-CA00633.
XX
PR 22-JUN-1998; 98US-0090276.
XX 03-JUL-1997; 97US-0051643.
XX 18-MAY-1998; 98US-0086020.
XX
PA (IDBI-) ID BIOMEDICAL CORP.
XX
PI Bekkaoui F, Cloney LP;

```

XX WP1: 1999-106072/09.
DR
XX
PT Method for determining the presence of an antibiotic resistant mecA
PT gene in a sample - using a scissile link containing nucleic acid
PT probe for antibiotic resistant mecA gene
XX
PS Claim 4; Page 17; 59pp; English.
XX
CC The present sequence represents a probe used for determining the
CC presence of an antibiotic resistant mecA gene in a biological sample.
CC The method provides a means for the rapid detection, for both
CC the prevention of transmission and treatment of, methicillin resistant
CC Staphylococcus species.
XX
SQ Sequence 108 BP: 53 A; 14 C; 16 G; 25 T; 0 other;
Query Match 100.0%; Score 20; DB 20; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 GTTACTGAAATATCTTGGC 20
|||||
Db 74 GTTACTGCAATATCTTGGC 55
RESULT 9
AAT04536/C
ID AAT04536 standard; cDNA to mRNA; 1789 BP.
XX
AC AAT04536;
XX
DT 11-APR-1996 (first entry)
XX
DE Staphylococcus aureus 'mecA' protein coding sequence.
XX
KW methicillin-resistant Staphylococcus aureus; MRSA; 'mecA' protein;
KW antibiotic resistance; ds.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT 1..1608
FT CDS /*tag= a
FT /product= 'mecA' protein
XX
FT JP07209294-A.
XX
PM 11-AUG-1995.
XX
PD 10-JAN-1994; 94JP-0012226.
XX
PR 10-JAN-1994; 94JP-0012226.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KAWA/) KAWANO M.
PA (MITU) MITSUBISHI CHEM CORP.
XX
XX WP1: 1995-313917/41.
DR P-PSDB; AAR80035.
XX
PT New 'mecA' protein and DNA encoding it - used for the detection of
PT methicillin-resistant Staphylococcus aureus
XX
PS Claim 5; Page 11-13; 15pp; Japanese.
XX
CC The present sequence codes for the 'mecA' protein which controls
CC methicillin resistance in methicillin-resistant Staph. aureus. The
CC 'mecA' protein (mol. wt. 40000) is useful for preparation of
CC antiserum specific for MRSA, thereby allowing methicillin-resistant
CC and methicillin-sensitive strains to be distinguished. The coding
CC sequence was obtained by PCR amplification of the mecA sequence
CC (see AAT04538) using primers AAT04537 and AAT04539.

CC N.B. In the sequence listing of the patent specification, the
CC sequence length is stated to be 1785 bp.
XX
SQ Sequence 1789 BP: 735 A; 263 C; 302 G; 489 T; 0 other;
Query Match 100.0%; Score 20; DB 16; Length 1789;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTACTGAAATATCTTGGC 20
|||||
Db 581 GTTACTGCAATATCTTGGC 562
RESULT 10
AAQ28599/C
ID AAQ28599 standard; DNA; 2007 BP.
XX
AC AAQ28599;
XX
DT 19-FEB-1993 (first entry)
XX
DE Encodes penicillin binding protein PBP2A-27R.
XX
KW penicillin; antibiotic; bacteria; methicillin; staphylococci;
KW soluble; chelating peptide; MRSA infection; methicillin resistant;
KW strain.
XX
OS Staphylococcus aureus strain 27R.
XX
FH Key Location/Qualifiers
FT 1..2007
FT CDS /*tag= a
XX
PM EP505151-A.
XX
PD 23-SEP-1992.
XX
PR 18-MAR-1992; 92EP-0302298.
XX
PR 19-MAR-1991; 91US-0672704.
XX
PA (ELL) LILLY & CO ILL.
XX
PI Blaszcak LC, Skatrud PL, Smith MC, Wu CYE;
XX
DR WP1: 1992-318034/39.
XX
PT Polynucleotide cpd. encoding PBP 2A-27R protein or its deriv. -
PT contains PBP isolated from staphylococcus aureus and is used to
PT treat methicillin resistant staphylococci
XX
PS Disclosure; Page 14; 101pp; English.
XX
CC This sequence encodes a PBP2A penicillin binding protein isolated
CC from S. aureus strain 27R. A cDNA library was constructed from
CC S. aureus DNA in lambda phage EMPL3. Packaging extracts from this
CC were then used to infect E. coli CJ236. Plaques were screened for the
CC presence of the mecA-27R gene by a probe produced by PCR amplification
CC of the mecA gene using primers Q28600.1. Positive plaques were purified
CC and digested with HindIII, and this fragment digested with XbaI and
CC cloned into M13amp18 and M13amp19 for sequencing.
XX
SQ Sequence 2007 BP: 855 A; 272 C; 341 G; 539 T; 0 other;
Query Match 100.0%; Score 20; DB 13; Length 2007;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTACTGAAATATCTTGGC 20
|||||
Db 980 GTTACTGCAATATCTTGGC 961

RESULT 11
 AAT28568/c
 ID AAT28568 standard: DNA; 2007 BP.
 XX
 AC AAT28568;
 XX
 DT 01-APR-1997 (first entry)
 XX
 DE Bacterial antibiotic resistance gene, mecA, probe.
 XX
 KW Detection; probe; amplification primer; bacterial pathogen; pneumonia;
 KW *Escherichia coli*; *Klebsiella pneumoniae*; *Pseudomonas aeruginosa*;
 KW *Proteus mirabilis*; *Streptococcus pneumoniae*; *Staphylococcus aureus*;
 KW *Staphylococcus epidermidis*; *Enterococcus faecalis*; respiratory tract;
 KW *Staphylococcus saprophyticus*; *Streptococcus pyogenes*; urinary tract;
 KW *Haemophilus influenzae*; *Moraxella catarrhalis*; septicæmia; meningitis;
 KW Infection; intra-abdominal infection; skin infection;
 KW bacterial resistance; beta-lactam antibiotic; ds.
 XX
 XX Synthetic.
 A
 PN W09608582-A2.
 XX
 PD 21-MAR-1996.
 XX
 PF 12-SEP-1995; 95WO-CA00528.
 XX
 PR 12-SEP-1994; 94US-0304732.
 XX
 PA (BERG/) BERGERON M. G.
 PA (QUEL/) QUELLETTE M.
 PA (ROY/) ROY P. H.
 XX
 PI Bergeron MG, Quellette M, Roy PH;
 XX
 DR WPI; 1996-179953/18.
 XX
 PT Method for the detection of bacterial species using probes and
 PT primers allows detection and quantification of antibiotic
 PT resistant bacteria in patients, the environment and food
 XX
 PS Claim 91; Page 144-145; 216pp; English.
 CC The sequences given in AAT28560-76 represent fragments derived from
 CC bacterial antibiotic resistance genes which were used as probes in the
 CC method of the invention for the detection of bacterial species in a
 CC sample. The method of the invention comprises using probes and/or
 CC amplification primers which are specific, ubiquitous and sensitive for
 CC determining the presence and/or amount of nucleic acids from selected
 CC bacterial species in any sample, where the bacterial nucleic acid
 CC comprises a selected target region hybridisable with the probes or
 CC primers. The method comprises contacting the sample with the probes
 CC or primers and detecting the presence and/or amount of hybridised
 CC primers or amplification products as and indication of the presence
 CC and/or amount of the bacterial species. This method may be used to
 CC detect commonly encountered bacterial pathogens, e.g. *Escherichia coli*,
 CC *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*,
 CC *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Staphylococcus*
 CC *epidermidis*, *Enterococcus faecalis*, *Staphylococcus saprophyticus*,
 CC *Streptococcus pyogenes*, *Haemophilus influenzae* and *Moraxella*
 CC *catarrhalis*. These bacterial species are associated with approx. 90% of
 CC urinary tract infections and with a high percentage of other severe
 CC infections including septicæmia, meningitis, pneumonia, intra-abdominal
 CC infections, skin infections and other severe respiratory tract
 CC infections. The method may also be used to evaluate a bacterial
 CC resistance to beta-lactam antibiotics.
 XX
 SO Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other.
 Query Match 100.0%; Score 20; DB 17; Length 2007;
 Best Local Similarity 100.0%; Pred. NO. 3.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY		1 GTTACTGCAATATCTTTGCC 20
Db	980 GTTAGTGGAATATCTTGCC 961	
	RESULT 12	
ID	AAV68337/c	
XX	AAV68337 standard; DNA; 2007 BP.	
AC	AAV68337;	
XX		
DE	21-JUN-1999 (first entry)	
XX		
KW	Penicillin binding protein PBP2A meca-27R gene of S. aureus 27R.	
XX		
OS	penicillin binding protein; PBP2A-27R; meca-27R gene; methicillin resistance; antibiotic; assay; purification; ss.	
PN	Staphylococcus aureus.	
XX	EP875578-A2.	
PD	04-NOV-1998.	
PF	18-MAR-1992; 92EP-0302298.	
PR	19-MAR-1991; 91US-0672704.	
PA	(EHLI) LILLY & CO ELI.	
P1	Biaszczak LC, Skatrud PL, Smith MC, Wu CE;	
DR	MPI; 1998-559443/48.	
XX	P-PSDB; AAM81149.	
PT	New Staphylococcus aureus soluble penicillin-binding proteins and their derivatives - useful for screening for compounds effective against methicillin resistant organisms	
PS	Disclosure; Page 14-16; 97pp; English.	
XX		
CC	This meca-27R gene encodes penicillin binding protein 2A (PBP2A-27R) responsible for the methicillin resistance of Staphylococcus aureus strain 27R. The invention provides new PBPs of formula SP-L-PBP2As, where: SP is 0 or a signal peptide (preferably from the ampC, ompA or beta-lactamase gene product); L is Met-Val or a compound of formula Met-Gly-C(=Pro)-PBP2As, where CP = 0 or a chelating peptide (see AAM81151-58) of formula (His)x(Aiy)-(His)z and A-an amino acid, x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above polypeptide where each monomer unit is the same or different; Pro is proline, n = 0 or 1; and PBP2As is soluble PBP2A-27R protein (see AAM81159-62). Also claimed are polynucleotides encoding specific soluble PBP2A compounds. The new PBP2A-27R proteins are useful for assaying for agents useful as antibiotics against methicillin resistant Staphylococcus strains by creating a kinetically inert complex between a support-immobilised transition ion and a modified soluble PBP2A protein comprising a chelating agent, which screens for agents which bind to PBP2A proteins (disclosed). Soluble forms of PBP2A-27R protein facilitate crystallisation as they lack their transmembrane association region, and so are useful for x-ray crystallography studies of the protein, assisting in the design of antibiotic compounds against methicillin resistant Staphylococcus strains (disclosed). The chelating peptide operably linked to the PBP2A-27R proteins is useful for purifying PBPs.	
SO	Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other:	
Query Match	100.0%; Score 20; DB 19; Length 2007;	
Best Local Similarity	100.0%; Pred. No. 3.6;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1 GTTAGTGGAATATCTTTGCC 20		


```

OS      Staphylococcus aureus.
XX      Key      Location/Qualifiers
FH      CDS      105..2110
FT      /*tag= a
XX      EP527628-A.
XX      17-FEB-1993.
XX      PD
XX      10-AUG-1992; 92EP-0307307.
XX      PE
XX      13-AUG-1991; 91US-0744770.
XX      PR
XX      (ELIL ) LILLY & CO ELL.
PA
XX      Skatrud PL, Unal S;
PI
XX      WPI: 1993-054352/07.
DR      P-PSDB; AAR30845.
XR
'
f      Detection of methicillin-resistant staphylococci - using
PT      polymerase chain reaction method, and DNA primers, for rapid,
PS      sensitive and accurate detection
XX      Disclosure: Pages 7-10; 16pp; English.
XX
CC      The inventors claim a method for detecting methicillin-resistant
CC      staphylococcal infections which involves the use of the PCR primed
CC      by fragments of the Staphylococcus meca gene. More specifically, the
CC      initial primers used are nucleotides 141-160 and the inverse
CC      complement of nucleotides 1929-1952 of the S. aureus meca gene. The
CC      interior primers are nucleotides 568-593 and the inverse complement
CC      of 1647-1670 of the S. aureus meca gene.
XX
SQ      Sequence 2110 BP; 896 A; 290 C; 350 G; 574 T; 0 other;
Query Match      100.0%; Score 20; DB 14; Length 2110;
Best Local Similarity 100.0%; Pred. No. 3 6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY      1 GTTAGTTGAATATCTTGCC 20
      ||||||||||||||||
Db      1084 GTTAGTTGAATATCTTGCC 1065

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Job time : 131.391 secs

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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:12:39 : Search time 27.2626 Seconds
(without alignments)
224.980 Million cell updates/sec

Title: US-09-865-579A-21

Perfect score: 20

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	2007	2	US-08-743-637B-169
C 2	20	100.0	2007	3	US-08-526-840B-169
C 3	20	100.0	2028	4	US-09-134-001C-1710
C 4	15.8	79.0	15393	4	US-09-453-702B-191
C 5	15.4	77.0	792	4	US-09-134-001C-2275
C 6	15.2	76.0	1348	4	US-08-936-165A-186
C 7	15.1	76.0	37948	4	US-09-251-645-11
C 8	14.8	74.0	489	4	US-09-812-484-30
C 9	14.4	72.0	1998	4	US-09-280-116-222
C 10	14.4	72.0	1998	4	US-09-332-295-3
C 11	14.4	72.0	3996	4	US-09-709-979-3
C 12	14.4	72.0	3996	4	US-09-208-742-1
C 13	14.4	72.0	3997	4	US-08-858-207A-262
C 14	14.2	71.0	571	4	US-08-858-207A-262
C 15	14.2	71.0	695	4	US-09-200-934-6
C 16	14.2	71.0	954	4	US-09-134-001C-1156
C 17	14.2	71.0	1029	4	US-09-134-001C-2361
C 18	14.2	71.0	1668	1	US-08-463-090B-1
C 19	14.2	71.0	1863	2	US-08-455-073A-3
C 20	14.2	71.0	2240	1	US-08-148-058A-12
C 21	14.2	71.0	2240	1	US-08-478-042-12
C 22	14.2	71.0	2240	1	US-08-645-215-12
C 23	14.2	71.0	2240	2	US-08-466-604-12
C 24	14.2	71.0	2291	2	US-08-725-736D-1
C 25	14.2	71.0	2291	3	US-09-162-368B-1
C 26	14.2	71.0	2291	3	US-09-161-877B-1
C 27	14.2	71.0	2304	1	US-08-464-266-1

C 28	14.2	71.0	2304	1	US-08-464-272-1	Sequence 1, Appl
C 29	14.2	71.0	2304	4	US-08-464-514-1	Sequence 1, Appl
C 30	14.2	71.0	2304	4	US-08-466-403-1	Sequence 1, Appl
C 31	14.2	71.0	3115	4	US-09-221-017B-849	Sequence 849, App
C 32	14.2	71.0	5224	4	US-09-033-428-2	Sequence 2, Appl
C 33	14.2	71.0	5224	4	US-09-033-556-5	Sequence 5, Appl
C 34	14.2	71.0	5278	4	US-08-961-527-227	Sequence 227, App
C 35	14.2	71.0	5365	4	US-08-961-527-77	Sequence 77, Appl
C 36	14.2	71.0	5917	4	US-09-780-175-17	Sequence 17, Appl
C 37	14.2	71.0	25165	4	US-09-453-702B-39	Sequence 39, Appl
C 38	14	70.0	393	2	US-08-853-659A-14	Sequence 14, Appl
C 39	14	70.0	639	4	US-09-221-017B-741	Sequence 741, App
C 40	14	70.0	15512	2	US-08-853-659A-5	Sequence 5, Appl
C 41	14	70.0	15512	2	US-08-853-659A-8	Sequence 8, Appl
C 42	14	70.0	15512	2	US-08-853-659A-63	Sequence 63, Appl
C 43	14	70.0	15512	2	US-08-853-659A-66	Sequence 66, Appl
C 44	14	70.0	24701	2	US-08-853-659A-2	Sequence 2, Appl
C 45	14	70.0	24701	2	US-08-853-659A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-743-637B-169/c
Sequence 169, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSER: OUALES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586, 90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ. ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0%; Score 20; DB 2; Length 2007;

Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGTGAATATCTTGCC 20
|||||
Db 980 GTTAGTGAATATCTTGCC 961

RESULT 2
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELETTE, Marc
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586, 90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169
Query Match 100.0%; Score 20; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGTGAATATCTTGCC 20
|||||
Db 980 GTTAGTGAATATCTTGCC 961
RESULT 3
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 20; DB 4; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTGAATATCTTGCC 20
|||||
Db 1001 GTTAGTGAATATCTTGCC 982

RESULT 4
US-09-453-702B-191/c
; Sequence 191, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blatner, Frederick R.
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: NO. 6365723e1 Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296, 95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15393
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 191:

US-09-453-702B-191

Query Match 79.0%; Score 15.8; DB 4; Length 15393;
 Best Local Similarity 89.5%; Pred. No. 56;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 TTAGTTGATATCTTGGCC 20

Db 746 TCAGTTGATATCTTGGCC 728

RESULT 5

US-09-134-001C-2275/c
 : Sequence 2275, Application US/09134001C
 : Patent No. 6380370
 : GENERAL INFORMATION:
 : APPLICANT: Lynn Doucelle-Stamm et al
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 : FILE REFERENCE: GTC-007
 : CURRENT APPLICATION NUMBER: US/09/134,001C
 : PRIOR FILING DATE: 1998-08-13
 : PRIOR APPLICATION NUMBER: US 60/064,964
 : PRIOR FILING DATE: 1997-11-08
 : PRIOR APPLICATION NUMBER: US 60/055,779
 : PRIOR FILING DATE: 1997-08-14
 : NUMBER OF SEQ ID NOS: 5674
 : SEQ ID NO 2275
 : LENGTH: 792
 : TYPE: DNA
 : ORGANISM: Staphylococcus epidermidis
 : US-09-134-001C-2275

Query Match 77.0%; Score 15.4; DB 4; Length 792;
 Best Local Similarity 94.1%; Pred. No. 68;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 ACTGTGATATCTTGGCC 20

Db 617 ACTGTGATATCTTGGCC 601

RESULT 6

US-08-936-165A-186/c
 : Sequence 186, Application US/08936165A
 : Patent No. 6348582
 : GENERAL INFORMATION:
 : APPLICANT: Black, Michael
 : APPLICANT: Burnham, Martin
 : APPLICANT: Hodgson, John
 : APPLICANT: Knowles, David
 : APPLICANT: Lonetto, Michael
 : APPLICANT: Nicholas, Richard
 : APPLICANT: Pratt, Julie
 : APPLICANT: Reichard, Richard
 : APPLICANT: Rosenberg, Martin
 : APPLICANT: Ward, Judith
 : TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
 : TITLE OF INVENTION: Polypeptides and Their Uses
 : NUMBER OF SEQUENCES: 534
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: SmithKline Beecham Corporation
 : STREET: 709 Swedeland Road
 : CITY: King of Prussia
 : STATE: PA
 : COUNTRY: USA
 : ZIP: 19406-0939
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FASTSEQ for Windows Version 2.0
 : CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/936,165A
 FILING DATE: 24-SEP-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/027,032
 FILING DATE: 24-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Glimm, Edward R.
 REGISTRATION NUMBER: 38,891
 REFERENCE/DOCKET NUMBER: P50549
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-4478
 TELEFAX: 610-270-5090
 TELEX:

INFORMATION FOR SEQ ID NO: 186:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1348 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: Genomic DNA
 : US-08-936-165A-186

Query Match 76.0%; Score 15.2; DB 4; Length 1348;
 Best Local Similarity 85.0%; Pred. No. 90;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTTAGTTGATATCTTGGCC 20

Db 559 GTTAGTTGATATCTTGGCC 540

RESULT 7

US-09-251-645-11/c
 : Sequence 11, Application US/09251645
 : Patent No. 6281413
 : GENERAL INFORMATION:
 : APPLICANT: Kramer, Vance C.
 : APPLICANT: Morgan, Michael K.
 : APPLICANT: Anderson, Arne R.
 : APPLICANT: Carl, Hope
 : APPLICANT: Warren, Gregory W.
 : APPLICANT: Dunn, Martha S.
 : APPLICANT: Chen, Jeng S.
 : TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
 : FILE REFERENCE: CGC1963//
 : CURRENT APPLICATION NUMBER: US/09/251,645
 : CURRENT FILING DATE: 99-02-17
 : NUMBER OF SEQ ID NOS: 11
 : SOFTWARE: FASTA
 : SEQ ID NO 11
 : LENGTH: 37948
 : TYPE: DNA
 : ORGANISM: Photorhabdus luminescens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (15171)..(18035)
 : OTHER INFORMATION: orf5
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (23768)..(31336)
 : OTHER INFORMATION: hpn2
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (31393)..(35838)
 : OTHER INFORMATION: orf2
 : US-09-251-645-11

Query Match 76.0%; Score 15.2; DB 4; Length 37948;
 Best Local Similarity 85.0%; Pred. No. 1,2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTTACTGATATCTTGGC 20
DB 33968 GTCACTGACATCTTGGC 33949

RESULT 8
US-09-812-484-30/C
Sequence 30, Application US/09812484
Patent No. 6444430
GENERAL INFORMATION:
APPLICANT: Stuart, Susan G.
APPLICANT: Au-Young, Janice
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Parvi
APPLICANT: Yue, Henry
TITLE OF INVENTION: NDR2-RELATED PROTEINS
FILE REFERENCE: PC-0038 CIP
CURRENT APPLICATION NUMBER: US/09/812,484
CURRENT FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL Program
SEQ ID NO 30
LENGTH: 489
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6444430 7019388966H1
US-09-812-484-30

Query Match 74.0%; Score 14.8; DB 4; Length 489;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTTACTGATATCTTGG 18
DB 113 GTTACTGATATCTGCTG 96

RESULT 9
PCT-US96-05320A-766
Sequence 766, Application PC/TUS9605320A
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences
APPLICANT: 9410 Key West Avenue
APPLICANT: Rockville, MD 20850
APPLICANT: United States of America
APPLICANT: Johns Hopkins University
APPLICANT: 720 Rutland Avenue
APPLICANT: Baltimore, MD 21205
APPLICANT: United States of America
APPLICANT: Mark D. Adams
APPLICANT: Owen White
APPLICANT: Hamilton O. Smith
TITLE OF INVENTION: J. Craig Venter
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome,
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20003-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05320A
FILING DATE: April 22, 1996
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Eric K. Steffe
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.014PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 766:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
PCT-US96-05320A-766

Query Match 72.0%; Score 14.4; DB 5; Length 645;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTAGTTGATATCTTT 17
DB 616 TTAGTTGATATCTTT 631

RESULT 10
US-09-280-116-222
Sequence 222, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 222
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: ubiquitin carboxyl-terminal hydrolases family 2
NAME/KEY: misc_feature
LOCATION: (1)..(1998)
OTHER INFORMATION: n - a, t, c or g
US-09-280-116-222

Query Match 72.0%; Score 14.4; DB 4; Length 1998;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTACTGATATCTTT 16
DB 1432 GTTACTGATATCTTT 1447

RESULT 11
US-09-332-295-3/C
Sequence 3, Application US/09332295
Patent No. 6303372
GENERAL INFORMATION:
APPLICANT: Kaufmann, Joerg
TITLE OF INVENTION: C1F130 INHIBITS CELL CYCLE PROGRESSION
FILE REFERENCE: 200130.456 / 1513.003
CURRENT APPLICATION NUMBER: US/09/332,295
CURRENT FILING DATE: 1999-06-11

```

:
:
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 3.0.
:
: SEQ ID NO 3
:
: LENGTH: 3996
:
: TYPE: DNA
:
: ORGANISM: Homo sapien
:
: US-09-332-295-3

```

Query Match:	72.0%:	Score 14.4:	DB 4:	Length 3996:
Host local Similarity:	93.8%:	Pred No. 2.4e+02:		
Matches 15, Conservative		0; Mismatches 1;	Indels 0;	Caps 0

OY	5	GTTGATATCTTGGC	20
Db	1814	GCTGAATATCTTTGCC	1799

RESULT 12
US-09-709-979-3/C
Sequence 3, Application US/09709979
Patent No. 6423822

```

1  APPLICANT: Kaufmann, Joerg
2  TITLE OF INVENTION: CIP130 INHIBITS CELL CYCLE PROGRESSION
3  FILE REFERENCE: 200130.456 / 1513.003
4  CURRENT APPLICATION NUMBER: US/09/709,979
5  CURRENT FILING DATE: 2000-11-09
6  PRIOR APPLICATION NUMBER: US 09/332,295
7  PRIOR FILING DATE: 1999-06-11
8  NUMBER OF SEQ ID NOS: 4
9  SOFTWARE: FastSeq for Windows Version 3.0
10 SEQ ID NO: 3
11     LENGTH: 3996
12     TYPE: DNA
13 ORGANISM: Homo sapien
14 US-09-709-979-3

```

Query Match:	72.0%	Score 14.4:	DB 4:	Length 3996:
Best Local Similarity:	93.8%	Pred. NO. 2.4e+02:		
Matches 15, Conservative	0:	Mismatches 1:	Indels 0:	Gaps 0:

QY	5	GTTGATATCTTGGC	20
Db	1814	GCTGAATATCTTGGC	1799

RESULT 13
US-09-208-742-1/c
Sequence 1, Application US/09208742

```

: APPLICANT: Kaufmann, Joerg
: TITLE OF INVENTION: CIP150/hTAFII150 is Necessary for Cel
: TITLE OF INVENTION: Cycle Progression
: FILE REFERENCE: 1453.002
: CURRENT APPLICATION NUMBER: US/09/208,742
: CURRENT FILING DATE: 1998-12-10
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 3997
: TYPE: DNA
: ORGANISM: human
: US-09-208-742-1

```

Query Match	72.0%	Score 14.4	DB 4	Length 3997
Best Local Similarity	93.8%	Pred. No. 2.4e+02		
Matches 15	Conservative 0	Mismatches 1	Indels 0	Gaps 0

QY 5 GTTGATATCTTGGC 20
| | | | | | | | | |
Db 1814 GCTGAATATCTTGGC 1799

RESULT 14
US-08-858-207A-262/c
; Sequence 262, Application US/08858207A

```

1  GENERAL INFORMATION:
2  APPLICANT: Black, Michael
3  APPLICANT: Hodgson, John
4  APPLICANT: Knowles, David
5  APPLICANT: Nicholas, Richard
6  APPLICANT: Stodola, Robert
7  TITLE OF INVENTION: No. 6348328e1 Compounds
8  NUMBER OF SEQUENCES: 552

```

ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939

```
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
```

```

? SOFTWARE: FastISO for Windows Version 2.0.0
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/858,207A
? FILING DATE: 09-MAY-1997
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
?

```

; APPLICATION NUMBER: 60/0176
 ; FILING DATE: 14-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:

; NAME: GIMMI, Edward R
 ; REGISTRATION NUMBER: 38,891
 ; REFERENCE/DOCKET NUMBER: P50475
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: 601-352-2200
TELEFAX: 601-352-2200
TELEX: 601-352-2200

```

? INFORMATION FOR SEQ ID NO: 262:
?
?     SEQUENCE CHARACTERISTICS:
?         LENGTH: 571 base pairs
?         TYPE: nucleic acid
?         STRANDEDNESS: single
?         TOPOLOGY: linear
?
?     MOLECULE TYPE: CDNA
?
US-08-858-207A-262

```

Query Match	71.0%	Score 14.2	DB 4	Length 571
Best Local Similarity	84.2%	Pred. No. 2.5e+02		
Matches 16; Conservative	0	Mismatches 3	Indels 0	Gaps 0

QY 2 TTAGTTGAATATCTTGGC 20
 |||||
 Db 428 TTGCTTAATATCATTTGCC 410

RESULT 15
US-09-200-934-6/c
; Sequence 6, Application US/09200934
; Patent No. 595433

```

; GENERAL INFORMATION:
;;
;; APPLICANT: Liu, Qiang
;; APPLICANT: Sommer, St
; TITLE OF INVENTION:

```

1	TITLE OF INVENTION:	SINGLE TUBE PCR ASSAY FOR DETECTION OF CHROMOSOMAL
2	TITLE OF INVENTION:	MUTATIONS: APPLICATION TO THE INVERSION HOTSPOT IN THE
3	TITLE OF INVENTION:	FACTOR VIII GENE INCLUDING OPTIONAL USE OF SUBCYCLING
4	TITLE OF INVENTION:	PCR

```

; CURRENT APPLICATION NUMBER: US/09/200,934
; CURRENT FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: 09/103,505

```

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; EARLIER FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 695
;
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-200-934-6

```

Query Match	71.0%;	Score 14.2;	DB 4	Length 695;
Best Local Similarity	84.2%;	Pred. No. 2.6e+02;		
Matches	16;	Conservative	0;	Mismatches 3;
				Indels 0;
				Gaps 0;
QY	1	GTACTGATATCTTGC	19	
Db	329	GTTCCTCTATATCTTGC	311	

Search completed: December 10, 2002, 22:54:33
 Job time : 37.3876 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 ; Search time 25.9218 Seconds
(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-21

Perfect score: 20

Sequence: 1 gtagtggaatattcttgc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	10	US-09-865-579A-11
2	20	100.0	20	10	US-09-865-579A-21
3	20	100.0	39	10	US-09-865-579A-28
4	20	100.0	2007	10	US-09-452-559-169
5	17.4	87.0	369	10	US-09-770-791-376
6	16.8	84.0	350	10	US-09-770-791-701
7	16.4	84.0	16484	10	US-09-070-927A-158
8	16.4	82.0	1374	9	US-09-938-842A-4922
9	15.8	79.0	19866	10	US-09-764-877-3887
10	15.4	77.0	442	10	US-09-924-035A-602
11	15.4	77.0	635	10	US-09-770-149-654
12	15.4	77.0	706	10	US-09-770-149-230
13	15.4	77.0	1200	10	US-09-887-576-739
14	15.4	77.0	2507	9	US-09-938-842A-4405
15	15.4	77.0	2507	10	US-09-925-301-397
16	15.2	76.0	699	10	US-09-815-242-4621
17	15.2	76.0	699	10	US-09-925-637-451
18	15.2	76.0	708	10	US-09-815-242-8576
19	15.2	76.0	708	10	US-09-815-242-8902

C 20	15.2	76.0	1348	10	US-09-939-980-186	Sequence 186, App
C 21	15.2	76.0	4431	10	US-09-817-514A-3	Sequence 3, Appl1
C 22	15.2	76.0	7053	10	US-09-070-927A-78	Sequence 78, Appl
C 23	15.2	76.0	12022	10	US-09-070-927A-117	Sequence 117, Appl
C 24	15.2	76.0	29607	10	US-09-764-877-3626	Sequence 3626, App
C 25	15	75.0	28	10	US-09-865-579A-22	Sequence 22, Appl
C 26	15	75.0	27360	10	US-09-070-927A-164	Sequence 164, App
C 27	14.8	74.0	87	10	US-09-864-761-19866	Sequence 19866, A
C 28	14.8	74.0	385	10	US-09-878-574-322	Sequence 322, App
C 29	14.8	74.0	391	10	US-09-878-574-3251	Sequence 3251, Ap
C 30	14.8	74.0	446	10	US-09-864-761-3285	Sequence 3085, Ap
C 31	14.8	74.0	507	10	US-09-783-590-6033	Sequence 6033, Ap
C 32	14.8	74.0	574	10	US-09-864-761-8082	Sequence 8082, Ap
C 33	14.8	74.0	1160	12	US-10-062-254-285	Sequence 285, App
C 34	14.8	74.0	3115	9	US-09-736-457-802	Sequence 802, App
C 35	14.8	74.0	3115	9	US-09-902-941-802	Sequence 802, App
C 36	14.8	74.0	3563	10	US-09-764-877-3956	Sequence 3956, Ap
C 37	14.8	74.0	4637	9	US-09-736-457-804	Sequence 804, App
C 38	14.8	74.0	4637	9	US-09-902-941-804	Sequence 804, App
C 39	14.8	74.0	32192	10	US-09-764-877-3657	Sequence 3657, Ap
C 40	14.6	73.0	7287	10	US-09-070-927A-210	Sequence 210, App
C 41	14.4	72.0	363	10	US-09-867-701-2366	Sequence 2366, App
C 42	14.4	72.0	500	10	US-09-917-800A-529	Sequence 529, App
C 43	14.4	72.0	2010	10	US-09-887-576-232	Sequence 232, Appl
C 44	14.4	72.0	3996	12	US-10-147-268-3	Sequence 3, Appl1
C 45	14.4	72.0	21761	10	US-09-764-847-1680	Sequence 1680, Ap

ALIGNMENTS

RESULT 1
US-09-865-579A-11
Sequence 11, Application US/09865579A
Patent No. US20020098492A1
GENERAL INFORMATION:
APPLICANT: Taya, Toshiki
APPLICANT: Ishiguro, Takahiko
APPLICANT: Saito, Junichi
TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
FILE REFERENCE: 9558-003-27
CURRENT APPLICATION NUMBER: US/09/865, 579A
PRIOR FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: JP 2000-163149
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-179394
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide capable of binding specifically to meca gene
US-09-865-579A-11
Query Match 100.0%: Score 20; DB 10; Length 20;
Best local similarity 100.0%: Pred. No. 0.4; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
Qy 1 GTTAGTTGAATATCTTGGC 20
Db 1 GTTAGTTGAATATCTTGGC 20
RESULT 2
US-09-865-579A-21
Sequence 21, Application US/09865579A
Patent No. US20020098492A1
GENERAL INFORMATION:

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: APPLICANT: Taya, Toshiki
: APPLICANT: Ishiguro, Takahiko
: TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
: TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
: FILE REFERENCE: 9558-003-27
: CURRENT APPLICATION NUMBER: US/09/865,579A
: CURRENT FILING DATE: 2001-05-29
: PRIOR APPLICATION NUMBER: JP 2000-163149
: PRIOR FILING DATE: 2000-05-29
: PRIOR APPLICATION NUMBER: JP 2000-179394
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 21
: LENGTH: 20
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Primer
: -09-865-579A-21

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Query Match          100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GTTAGTGAATATCTTTGCC 20

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RESULT 3
US-09-865-579A-28
: Sequence 28, Application US/09865579A
: Patent No. US20020098492A1
: GENERAL INFORMATION:
: APPLICANT: Taya, Toshiki
: APPLICANT: Ishiguro, Takahiko
: APPLICANT: Saito, Juichi
: TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
: TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
: FILE REFERENCE: 9558-003-27
: CURRENT APPLICATION NUMBER: US/09/865,579A
: CURRENT FILING DATE: 2001-05-29
: PRIOR APPLICATION NUMBER: JP 2000-163149
: PRIOR FILING DATE: 2000-05-29
: PRIOR APPLICATION NUMBER: JP 2000-179394
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 28
: LENGTH: 39
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Probe
US-09-865-579A-28

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Query Match          100.0%; Score 20; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTAGTGAATATCTTTGCC 20
DB 1 GTTAGTGAATATCTTTGCC 20

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RESULT 4
US-09-452-599-169/c
: Sequence 169, Application US/09452599
: Patent No. US20020055101A1
: GENERAL INFORMATION:
: APPLICANT: Bergeron, Michel G.

```

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: APPLICANT: Ouellette, Marc
: APPLICANT: Roy, Paul H.
: TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
: TITLE OF INVENTION: To Rapidly Detect and Identify Common Bacterial
: TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
: TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
: FILE REFERENCE: 12287/31
: CURRENT APPLICATION NUMBER: US/09/452,599
: CURRENT FILING DATE: 1999-12-01
: PRIOR APPLICATION NUMBER: 08/526,840
: PRIOR FILING DATE: 1995-09-11
: PRIOR APPLICATION NUMBER: 08/304,732
: PRIOR FILING DATE: 1994-09-12
: NUMBER OF SEQ ID NOS: 177
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 169
: LENGTH: 2007
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
US-09-452-599-169

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Query Match          100.0%; Score 20; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTTAGTGAATATCTTTGCC 20
DB 980 GTTAGTGAATATCTTTGCC 961

```

```

RESULT 5
US-09-770-791-376/c
: Sequence 376, Application US/09770791
: Patent No. US20020062014A1
: GENERAL INFORMATION:
: APPLICANT: Goriach, Jorn
: APPLICANT: An, Yong-Qiang
: APPLICANT: Hamilton, Carol M.
: APPLICANT: Price, Jennifer L.
: APPLICANT: Raines, Tracy M.
: APPLICANT: Yu, Yang
: APPLICANT: Rameaka, Joshua G.
: APPLICANT: Page, Amy
: APPLICANT: Matthew, Abraham V.
: APPLICANT: Ledford, Brooke L.
: APPLICANT: Woessner, Jeffrey P.
: APPLICANT: Haas, William David
: APPLICANT: Garcia, Carlos A.
: APPLICANT: Krieker, Maja
: APPLICANT: Slader, Ted
: APPLICANT: Davis, Keith R.
: APPLICANT: Allen, Keith
: APPLICANT: Hollman, Neil
: APPLICANT: Hurban, Patrick
: TITLE OF INVENTION: Expressed Sequences of Arabidopsis
: TITLE OF INVENTION: thaliana
: FILE REFERENCE: 2029 (PARA-018PRV)
: CURRENT APPLICATION NUMBER: US/09/770,791
: CURRENT FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/178,480
: PRIOR FILING DATE: 2000-01-27
: NUMBER OF SEQ ID NOS: 999
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 376
: LENGTH: 369
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(369)
: OTHER INFORMATION: n - A,T,C or G
US-09-770-791-376

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OY 2 TTACTGATATCTTGC 19
Db 1338 TTACTGATATCTTGC 1355

RESULT 9

US-09-764-877-3887
Sequence 3887, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3887
LENGTH: 19866
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-3887

Query Match 79.0%; Score 15.8; DB 10; Length 19866;
Best Local Similarity 89.5%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTTAGTGATATCTTGC 19
Db 1311 GTTAGTGATATCTTGC 1329

RESULT 10

US-09-924-035A-602
Sequence 602, Application US/09924035A
Patent No. US20020142319A1
GENERAL INFORMATION:
APPLICANT: Grilach, Jörn
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2011US
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/148,784
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 602
LENGTH: 442
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-924-035A-602

Query Match 77.0%; Score 15.4; DB 10; Length 442;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTACTGATATCTTGC 18
Db 80 TTGGTTGATATCTTGC 96

RESULT 11

US-09-770-149-654/C
Sequence 654, Application US/09770149
Patent No. US20020059663A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jörn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.

APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Mathew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Woessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krickler, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 654
LENGTH: 635
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-770-149-654

Query Match 77.0%; Score 15.4; DB 10; Length 635;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTACTGATATCTTGC 18
Db 556 TTGGTTGATATCTTGC 540

RESULT 12

US-09-770-149-654/C
Sequence 230, Application US/09770149
Patent No. US20020059663A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jörn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Mathew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Woessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krickler, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 230
LENGTH: 706

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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-230

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 10; Length 706;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 TACTGCAATATCTTTGC 19
    ||||| ||||| |||||
Db 106 TACTTGAATACTTTGC 90

RESULT 13
US-09-887-576-739
; Sequence 739, Application US/09887576
; Patent No. US2002014407A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001U1
; CURRENT APPLICATION NUMBER: US/09/887,576
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 739
; LENGTH: 1200
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-739

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 10; Length 1200;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTACTGCAATATCTTTG 18
    ||||| ||||| |||||
Db 697 TTACTTGAATATCTTTG 713

RESULT 14
US-09-938-842A-4405
; Sequence 4405, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepes, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
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; SEQ ID NO 4405
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4405

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 9; Length 2000;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTACTGCAATATCTTTG 18
    ||||| ||||| |||||
Db 1500 TTACTTGAATATCTTTG 1516

RESULT 15
US-09-925-301-397
; Sequence 397, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1684
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 397
; LENGTH: 2507
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2469)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2496)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2504)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2505)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-397

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 10; Length 2507;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 AGTGAATATCTTTGCC 20
    ||||| ||||| |||||
Db 877 AGTTGAAGATCTTTGCC 893
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Search completed: December 11, 2002, 06:07:24
Job time : 31.9218 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 : Search time 1076.75 Seconds
(without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579A-20

Perfect score: 21

Sequence: 1 tttctttctctcataatg 21

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
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22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_pod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.4	92.4	459	17	A2792877
2	19.4	92.4	554	17	A2792877
3	18.4	87.6	107	13	A2271915
4	18.4	87.6	183	9	B3391473
5	18.4	87.6	232	17	AA481540
6	18.4	87.6	320	9	AA481540

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL COMMENT
A2792877	LOCUS	2M0045107R Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG2M0045107 R, DNA sequence.	A2792877	A2792877.1	GI:12937256	GSS.	house mouse.	1 (bases 1 to 459)	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid Inserts	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL COMMENT
A2792877	LOCUS	2M0045107R Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG2M0045107 R, DNA sequence.	A2792877	A2792877.1	GI:12937256	GSS.	house mouse.	1 (bases 1 to 459)	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid Inserts	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00

Plate: 0045 row: 1 column: 07
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 459.
 Location/Qualifiers
 1..459
 source

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U06C2M0045107"
 /clone_1lb="Mouse 10kb plasmid U06C1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b|Ap129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 168 a 67 c 70 g 154 t
 ORIGIN
 Query Match 92.4%; Score 19.4; DB 17; Length 459;
 Best Local Similarity 95.2%; Pred. No. 3e+04;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21
 |||||
 Db 68 TTTTCTTTTCTCTATTATG 88

RESULT 2
 A2271915 554 bp DNA linear GSS 26-JUL-2000
 LOCUS
 DEFINITION
 ' DNA sequence.
 A2271915
 ' A2271915.1 GI:9485532

CESSION
 KEYWORDS
 SOURCE
 ORGANISM
 house mouse.
 Mus musculus

REFERENCE
 AUTHORS
 B. Levin, M., McGann, S., Tsegaye, G., Geer, K., Kroll, M., de Jong, P., and Fraser, C. M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other_GSSs: RPCI-23-146L23.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@ligr.org

TITLE
 JOURNAL
 COMMENT
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
 or from Resea ch Genetics (info@resgen.com). BAC end page:
 http://www.ligr.org/cdb/bac_ends/mouse/bac_end_intro.html
 Plate: 146 row: 1 column: 23
 Seq primer: SP6
 Class: BAC ends.
 Location/Qualifiers
 1..554
 source

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-146L23"
 /clone_1lb="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site: 1; EcoRI; Site: 2; EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 127 a 123 c 136 g 168 t
 ORIGIN

Query Match 92.4%; Score 19.4; DB 17; Length 554;
 Best Local Similarity 95.2%; Pred. No. 2.7e+04;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21
 |||||
 Db 409 TTTTCTTTTCTCTATTATG 429

RESULT 3
 BJ391473/c 107 bp mRNA linear EST 08-MAR-2002
 LOCUS
 DEFINITION
 BJ391473 Dictyostellium discoideum cDNA library, SF Dictyostellium
 discoidium cDNA clone dds24e03 5', mRNA sequence.
 BJ391473
 VERSION
 BJ391473.1 GI:19302559
 KEYWORDS
 SOURCE
 ORGANISM
 Dictyostellium discoideum.
 Dictyostellium discoideum

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
 1 (bases 1 to 107)
 Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
 Full length cDNA of Dictyostellium discoideum at the slug stage
 Unpublished (2002)
 Contact: Tadasi Shin-i
 Center for Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.

FEATURES
 source
 1..107
 Location/Qualifiers

/organism="Dictyostellium discoideum"
 /strain="AX4"
 /db_xref="taxon:44689"
 /clone="dds24e03"
 /clone_1lb="Dictyostellium discoideum cDNA library, SF"
 /sex="mat A"
 /dev_stage="Slug stage"
 BASE COUNT 64 a 0 c 9 g 34 t
 ORIGIN

Query Match 87.6%; Score 18.4; DB 13; Length 107;
 Best Local Similarity 95.0%; Pred. No. 1e+05; 1; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAT 20

Db	107	TTTTTTTCTGTATTAAAT	88
RESULT 4			
LOCUS		AA481540	
DEFINITION		aa35fi12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815279 3', mRNA sequence.	
ACCESSION		AA481540	
VERSION		AA481540.1	
KEYWORDS		EST.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		1 (bases 1 to 183)	
TITLE		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
JOURNAL		National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
COMMENT		Unpublished (1997)	
		Contact: Robert Strausberg, Ph.D.	
		Email: cgabs-remail.nih.gov	
		Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.	
		cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.	
		cDNA Library Arrayed by: Greg Lennon, Ph.D.	
		DNA Sequencing by: Washington University Genome Sequencing Center	
		Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLB at:	
		www.bio.lnl.gov/bdtp/image/image.html	
		Seq primer: -41m13 fwd. Et from Amersham	
		High quality sequence stop: 176.	
FEATURES		Location/Qualifiers	
SOURCE		1..183	
		/organism="Homo sapiens"	
		/db_xref="taxon:6034365"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:815279"	
		/clone_id="NCI-CGAP_GCB1"	
		/lissue_type="germlinal center B cell"	
		/lab_host="DH10B"	
		/note="vector: pRTT3D-Pac (Pharmacia) with a modified polylinker site_1; Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI). Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer	
		15'-TGTTACCAATCTGCAGTCGGACGCCGCCCTCATTTTCTTTTCTTTT-3'	
] Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."	
BASE COUNT		58 a 35 c 34 g 56 t	
ORIGIN			
Query Match		87.6%;	Score 18.4;
Best Local Similarity		95.0%;	Pred. No. 8.1e+04;
Matches 19;		Conservative 0;	Mismatches 1;
		Indels 0;	Gaps 0;
OY	1	TTTTCTTTCTGTATTAAAT	20
Db	6	TTTTCTTTCTGTATTAAAT	25
RESULT 5			
LOCUS		AZ033426	
DEFINITION		RPC1-23-361NZ.TJ RPC1-23 Mus musculus genomic clone RPC1-23-361NZ, DNA sequence.	
		232 bp	DNA linear
		GSS 01-MAR-2000	

ACCESSION	AZ033426
VERSION	AZ033426.1 GI:7117769
KEYWORDS	GSS.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 232)
AUTHORS	Zhao,S., Niemman,W.J., Feldblum,T., Malek,J., Shatsman,S., Akınret ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P and Fraser,C.M.
TITLE	Mouse BAC End Sequences from Library RPCI-23
JOURNAL	Unpublished (1999)
COMMENT	Other GSSs: RPCI-23-361N2.TV Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhaoc@tigr.org Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pietere@jmg.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 361 row: N column: 2 Seq primer: SP6 Class: BAC ends. Location/Qualifiers 1..232 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="RPCI-23-361N2" /clone_1lb="RPCI-23" /sex="Female" /lab_host="DH10B" /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1: EcoRI; Site 2: EcoRI; Female C57Bl/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
BASE COUNT	40 a 35 c 23 g 130 t 4 others
ORIGIN	
Query Match	87.6%; Score 18.4; DB 17; Length 232;
Best Local Similarity	95.0%; Pred. No. 7.3e+04;
Matches	19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 TTTCTTTTCTCATTAAT 20
Dd	48 TTTCTTTTCTTTATTAAAT 67
RESULT 6	
LOCUS	AU271259 320 bp mRNA linear EST 10-MAY-2002
DEFINITION	AU271259 VS Dictyostellium discoideum cDNA clone VSK473 3', mRNA
ACCESSION	AU271259
VERSION	AU271259
KEYWORDS	sequence.
SOURCE	AU271259.1 GI:20530057
ORGANISM	EST.
REFERENCE	Dictyostelium discoideum.
AUTHORS	Eukaryota; Mycetozoa; Dictyostelidiae; Dictyostellium. 1 (bases 1 to 320) Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE	Polymerase chain reaction analysis of cDNAs from unicellular and multicellular

JOURNAL COMMENT

stages of Dictyostelium discoideum
Unpublished (2002)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES

location/Qualifiers

BASE COUNT 126 a 43 c 33 g 90 t 28 others
ORIGIN /organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSK473"
/clone_id="VS"
/sex="mat A"
/dev_stage="vegetative"

Query Match

Best Local Similarity 87.6%; Score 18.4; DB 9; Length 320;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTAT 20
||||| ||||| ||||| |||||
Db 49 TTTCTTTTCTCTATTAT 68

RESULT 7

LOCUS AO236558/c 322 bp DNA linear GSS 29-SEP-1998
DEFINITION HS_2033_B2_F05_r7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2033 COL=10 Row=L, DNA sequence.

ACCESSION AO236558
VERSION AO236558.1 GI:3661959
KEYWORDS GSS.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 322)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589

CONTACT: Mahairas GC, Wallace JC, Hood L,
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2033 row: L column: 10
Class: BAC ends
High quality sequence stop: 322.

FEATURES

Location/Qualifiers

BASE COUNT 121 a 58 c 42 g 101 t
ORIGIN /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-2033 COL=10 Row=L"
/clone_id="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeLoBAC11, BAC clones in
E-Coli DH10B"

Query Match 87.6%; Score 18.4; DB 17; Length 322;
Best Local Similarity 95.0%; Pred. No. 6.3e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTAT 20
||||| ||||| ||||| |||||
Db 52 TTTCTTTTCTCTATTAT 33

RESULT 8

LOCUS AU271258 325 bp mRNA linear EST 10-MAY-2002
DEFINITION AU271258 VS Dictyostelium discoideum cDNA clone VSK473 5', mRNA
sequence.

ACCESSION AU271258
VERSION AU271258.1 GI:20530056
KEYWORDS EST.
SOURCE Dictyostelium discoideum.

ORGANISM

Dictyostelium discoideum.
Eukaryota; Mycelozoa; Dictyostellida; Dictyostelium.

REFERENCE

1 (bases 1 to 325)
Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
Takeuchi,I., Kohara,Y. and Tanaka,Y.
Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum

JOURNAL COMMENT

Unpublished (2002)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES

location/Qualifiers

BASE COUNT 126 a 45 c 35 g 105 t 14 others
ORIGIN /organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSK473"
/clone_id="VS"
/sex="mat A"
/dev_stage="vegetative"

Query Match 87.6%; Score 18.4; DB 9; Length 325;
Best Local Similarity 95.0%; Pred. NO. 6.3e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTAT 20
||||| ||||| ||||| |||||
Db 51 TTTCTTTTCTCTATTAT 70

RESULT 9

LOCUS BJ336009 358 bp mRNA linear EST 05-MAR-2002
DEFINITION BJ336009 Dictyostelium discoideum cDNA library, Ar Dictyostelium
discoideum cDNA clone dda52k07 5', mRNA sequence.

ACCESSION BJ336009
VERSION BJ336009.1 GI:19166139
KEYWORDS EST.

SOURCE

Dictyostelium discoideum.

ORGANISM

Dictyostelium discoideum.
Eukaryota; Mycelozoa; Dictyostellida; Dictyostelium.

REFERENCE

1 (bases 1 to 358)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
Full length cDNA of Dictyostelium discoideum at the aggregation
stage

JOURNAL COMMENT

Unpublished (2002)
Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshinigenes.nig.ac.jp.
Location/Qualifiers

FEATURES

source

1.358

/organism="Dicyostelium discoideum"

/strain="AX4"

/db_xref="taxon:44689"

/clone_lib="Dicyostelium discoideum cDNA library, AF"

/sex="mat A"

/dev_stage="Aggregation stage"

BASE COUNT 144 a 53 c 35 g 106 t 20 others

ORIGIN

Query Match 87.6%; Score 18.4; DB 13; Length 358;
Best Local Similarity 95.0%; Pred. No. 6e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TTTCTTTTCTCTATTAT 20

|||||

82 TTTTCTTTCTCTATTAT 101

RESULT 10 379 bp DNA linear GSS 09-MAY-2000
LOCUS RPCI-23-469P1.TJ RPCI-23 Mus musculus genomic clone RPCI-23-469P1,
DEFINITION DNA sequence.
ACCESSION A2111107
VERSION A2111107.1 GI:7764165
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 379)
AUTHORS Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akilret,
B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from library RPCI-23
Unpublished (1999)
Other-GSS: RPCI-23-469P1.TV

TITLE JOURNAL
COMMENT Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)
or from Resea ch Genetics ([inf@resgen.com](http://www.tigr.org/cdb/bac/ends/mouse/bac_end_intro.html)). BAC end page:
http://www.tigr.org/cdb/bac/ends/mouse/bac_end_intro.html
Plate: 469 row: P column: 1
Seq primer: SP6
Class: BAC ends.

FEATURES
source Location/Qualifiers
1.379
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="RPCI-23-469P1"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site: 1;
EcoRI; Site: 2; EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size

BASE COUNT 67 a 86 c 46 g 180 t

ORIGIN

Query Match 87.6%; Score 18.4; DB 17; Length 379;
Best Local Similarity 95.0%; Pred. No. 5.8e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTAT 20

|||||

94 TTTCTTTTCTCTATTAT 113

RESULT 11 392 bp mRNA linear EST 22-NOV-2000
LOCUS BF354467/c
DEFINITION MR2-HT0758-070800-009-e05 HT0758 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF354467
VERSION BF354467.1 GI:11313541
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 392)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Birones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE JOURNAL
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-HT0758-070800-009-e05&t3=2000-08-07&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 391.
Location/Qualifiers

FEATURES
source Location/Qualifiers
1.392
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0758"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site: 1; SmaI;
Site: 2; SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 120 a 81 c 103 t 1 others
ORIGIN
Query Match 87.6%; Score 18.4; DB 12; Length 392;
Best Local Similarity 95.0%; Pred. No. 5.8e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTTCTTTTCTCTATTAT 21

```

Db      51 TTTCTTATCTCTATTATG 32
|||||
RESULT 12
LOCUS   A2281155
DEFINITION A2281155 416 bp DNA linear GSS 26-JUL-2000
          RPCI-23-138B7.TJ RPCI-23 Mus musculus genomic clone RPCI-23-138B7,
          DNA sequence.
ACCESSION A2281155
VERSION   A2281155.1 GI:9500057
KEYWORDS GSS.
SOURCE    house mouse.
          ORGANISM Mus musculus
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 416)
AUTHORS   Zhao,S., Nierman,W., Feldblum,T., Malek,J., Shatsman,S., Anret,
          ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
          and Fraser,C.M.
          Mouse BAC End Sequences from Library RPCI-23
          Unpublished (1999)
          Other_GSS: RPCI-23-138B7.TV
          COMMENT Contact: Shaying Zhao
          Department of Eukaryotic Genomics
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0200
          Fax: 301 838 0208
          Email: szhao@tigr.org
          Clones are derived from the mouse BAC library RPCI-23. For BAC
          library availability, please contact Pieter de Jong
          (pieter@edjong.med.buffalo.edu). Clones may be purchased from
          BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
          or from Resea ch Genetiics (info@resgen.com). BAC end page:
          http://www.tigr.org/tdb/bac-ends/mouse/bac_end_intro.html
          Plate: 138 row: B column: 7
          Seq primer: SP6
          Class: BAC ends.
FEATURES
Source Location/Qualifiers
1..416
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-138B7"
/clone_11b="RPCI-23"
/sex="female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site_1:
EcoRI; Site_2: EcoRI; female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBAC3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 124 a 80 c 66 g 146 t
ORIGIN
Query Match 87.6%; Score 18.4; DB 17; Length 416;
Best Local Similarity 95.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 TTTCTTTTCTCTATTAT 20
Db 269 TTTCTTTTCTCTACTAT 288

```

```

VERSION BG238677.1 GI:12773750
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
          Glycine.
REFERENCE 1 (bases 1 to 438)
AUTHORS   Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
          ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
          Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,N., Bowers
          ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
          ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
          ,R., Waterston,R. and Wilson,R.
          Public Soybean EST Project
          Unpublished (1999)
          COMMENT Contact: Shoemaker R/Public Soybean EST Project
          Public Soybean EST Project
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          This clone is available through: ResGen, Invitrogen Corp. 2130
          South Memorial Parkway Huntsville, AL 35801 For further information
          call: (800)-533-4363 or contact via email: ccuteresgen.com.
FEATURES
Source Location/Qualifiers
1..438
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1043-3121"
/clone_11b="Gm-c1043"
/lisseq_type="Hypocotyl and Plumule, germinating seeds"
/lab_host="DH10B"
/note="vector: pRT3pac (Pharmacia); Site_1: EcoRI;
Site_2: NotI; This cDNA library was constructed from mRNA
isolated from hypocotyl and plumule tissues of seeds
germinated for three days of the cultivar Williams.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a NotI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by digestion with EcoRI and NotI. The
cDNA fragments were directionally cloned into the
EcoRI-NotI restriction site of the pRT3-Pac vector. The
ligated cDNA fragments were transformed into DH10B host
cells (Gibco BRL). This library was constructed by Dr.
Randy Shoemaker."
BASE COUNT 124 a 73 c 85 g 155 t 1 others
ORIGIN
Query Match 87.6%; Score 18.4; DB 12; Length 438;
Best Local Similarity 95.0%; Pred. No. 5.5e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 TTTCTTTTCTCTATTAT 20
Db 61 TTTCTTTTCTCTATTAT 80

```

```

RESULT 13
LOCUS   BG238677
DEFINITION BG238677 438 bp mRNA linear EST 28-NOV-2001
          sab54b01.v1 Gm-c1043 glycine max cDNA clone GENOME SYSTEMS CLONE
          ID: Gm-c1043-3121 5', mRNA sequence.
ACCESSION BG238677

```

```

RESULT 14
LOCUS   BJ354059/c
DEFINITION BJ354059 Dicotyledonum discoidium cDNA library, Af Dicotyledonum
          discoidium cDNA clone dda32k07 3', mRNA sequence.
ACCESSION BJ354059
VERSION   BJ354059.1 GI:19253653
KEYWORDS EST.
SOURCE    Dicotyledonum discoidium.
          ORGANISM Dicotyledonum discoidium
          Eukaryota; Mycetozoa; Dicotyledonidae; Dicotyledonum.
REFERENCE 1 (bases 1 to 438)
          Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.

```

```

TITLE      Full length cDNA of Dictyostelium discoideum at the aggregation
            stage
JOURNAL    Unpublished (2002)
COMMENT    Contact: Tadasi Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshin@genes.nig.ac.jp.
            Location/Qualifiers
FEATURES   1..438
            source
            /organism="Dictyostelium discoideum"
            /strain="AX4"
            /db_xref="taxon:44689"
            /clone="ddas2k07"
            /clone_lib="Dictyostelium discoideum cDNA library, AF"
            /sex="mat A"
            /dev_stage="Aggregation stage"
            /dev_stage="Aggregation stage"
BASE COUNT 133 a 41 c 59 g 204 t 1 others
IGIN

Query Match      87.6%; Score 18.4; DB 13; Length 438;
Best Local Similarity 95.0%; Pred. No. 5.5e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 TTTCTTTTCTCTATTAAAT 20
        |||||
Db      357 TTTTCTTTCTCTATTAAAT 338

RESULT 15
AO363486/c 439 bp DNA linear GSS 16-DEC-1999
LOCUS      nbxb0059C14r CUGI Rice BAC library Oryza sativa genomic clone
DEFINITION nbxb0059C14r, DNA sequence.
ACCESSION  AO363486
VERSION     AO363486
KEYWORDS   GSS.
SOURCE      Oryza sativa.
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 439)
            Wing,R.A. and Dean,R.A.
            A BAC End Sequencing Framework to Sequence the Rice Genome
            Unpublished (1998)
            On Dec 15, 1999 this sequence version replaced gl:4213141.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: twing@clemson.edu
            Seq primer: GGAAACAGCTATGACCATG
            Class: BAC ends
            High quality sequence stop: 339.
            Location/Qualifiers
FEATURES   1..439
            source
            /organism="Oryza sativa"
            /strain="Japonica"
            /cultivar="Nipponbare"
            /db_xref="taxon:4530"
            /clone="nbxb0059C14r"
            /clone_lib="CUGI Rice BAC Library"
            /tissue_type="leaf"
            /lab_host="E. coli DH10B"
            /note="Vector: pBelobAC11; site_1: HindIII; site_2:
            HindIII; Rice is one of two most popular grains in the
            world. Half of the world population especially those
            inhabiting highly populated areas of the humid tropics

```

and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

```

BASE COUNT 174 a 69 c 90 g 106 t
IGIN

Query Match      87.6%; Score 18.4; DB 17; Length 439;
Best Local Similarity 95.0%; Pred. No. 5.5e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 TTTCTTTTCTCTATTAAAT 20
        |||||
Db      357 TTTTCTTTCTCTATTAAAT 338

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Search completed: December 10, 2002, 22:49:55
 Job time : 1080.75 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:03:28 : Search time 182.547 Seconds
(without alignments)
345.422 Million cell updates/sec

Title: US-09-865-579A-25

Perfect score: 28

Sequence: 1 caactaactatgatgctaagaattcaaa 28

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

otal number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

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21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	28	ABK85925	Methicillin resist
2	28	100.0	28	AAK15487	Probe mecA913-1020
3	28	100.0	1789	AAK04536	Staphylococcus aur
4	28	100.0	2007	AAQ28599	Encodes penicillin
5	28	100.0	2007	AAK28568	Bacterial antibiotic
6	28	100.0	2007	AAV68337	Antibiotic binding
7	28	100.0	2007	ABA6993	Antibiotic binding
8	28	100.0	2028	ABN92247	Staphylococcus epi
9	28	100.0	2110	AAO35213	Sequence of the me

10	28	100.0	2322	13	AAQ25805	PBP2', Synthetic.
11	28	100.0	2455	16	AAK04538	Staphylococcus aur
12	28	100.0	2456	22	AAH01187	Staphylococcus aur
13	25	89.3	89	20	AAK05906	Oligonucleotide pro
14	25	89.3	89	20	AAK15478	Probe mecA945-89
15	20.6	73.6	13206	19	AAV52166	Streptococcus pneu
16	20.6	73.6	16995	19	AAV52215	Streptococcus pneu
17	20	71.4	1166	21	AAK47557	Streptococcus pneu
18	20	71.4	1168	21	AAK34492	Arabidopsis thalia
19	19.6	70.0	2229	21	AAK39154	Arabidopsis thalia
20	19	67.9	737	24	ABN68422	Streptococcus poly
21	19	67.9	247	20	AAK99638	Nucleic acid seque
22	19	67.9	1635	20	AAK99510	Nucleic acid seque
23	19	67.9	2996	19	AAV52293	Streptococcus pneu
24	19	67.9	11309	19	AAV52241	Streptococcus pneu
25	19	67.9	12505	23	ABK07020	Streptococcus pneu
26	19	67.9	134499	21	AAK22286	BAC containing rep
27	18.8	67.1	5711	24	ABO71041	Listeria monocytog
28	18.8	67.1	2944528	24	ABO3041	Listeria monocytog
29	18.8	67.1	3011208	24	ABO69245	Listeria innocua D
30	18.6	66.4	336	22	AAK39087	Novel human diago
31	18.6	66.4	2529	23	ABL19336	Drosophila melanoq
32	18.6	66.4	2821	23	ABL19338	Drosophila melanoq
33	18.6	66.4	3094	23	ABL27444	Drosophila melanoq
34	18.6	66.4	7962	23	ABL1516	Drosophila melanoq
35	18.6	66.4	7962	23	ABL19762	Drosophila melanoq
36	18.6	66.4	11443	19	AAV52182	Streptococcus pneu
37	18.4	65.7	1208	21	AAK3603	Arabidopsis thalia
38	18.4	65.7	4404	23	ABL29720	Drosophila melanoq
39	18.4	65.7	4622	24	ABK81410	DNA encoding small
40	18.4	65.7	6084	23	ABK12230	Drosophila melanoq
41	18.4	65.7	8076	24	ABK39955	Human chemically p
42	18.4	65.7	8136	24	ABK39957	Human chemically p
43	18.4	65.7	8136	24	ABL32555	Human immune syste
44	18	64.3	462	24	ABL3633	Human immune syste
45	18	64.3	588	24	ABQ27036	Oligonucleotide fo

ALIGNMENTS

RESULT 1

ID ABK85925 standard; DNA; 28 BP.

ABK85925:

16-AUG-2002 (first entry)

Methicillin resistant Staphylococcus aureus detection primer #25.

Methicillin resistant Staphylococcus aureus; MRSA; primer; ss:

mecA: probe.

OS Staphylococcus aureus.

PN EPI160333-A2.

PD 05-DEC-2001.

PF 29-MAY-2001; 2001EP-0112100.

PR 29-MAY-2000; 2000UP-0163149.

PR 09-JUN-2000; 2000UP-0179394.

(TOYJ) TOSOH CORP.

Taya T, Ishiguro T, Saito J;

WPI: 2002-395832/43.

New oligonucleotide specific for the mecA methicillin-resistance gene, useful for cleavage, detection and amplification of the gene or related

```

PT mRNA -
XX Claim 6; Page 21; 28pp; English.
PS
XX
CC This invention relates to oligonucleotides used for cleaving, detecting
CC and amplifying the mecA gene (associated with methicillin resistance in
CC Staphylococcus aureus) or its derived RNA. The invention also comprises
CC a detection method employing an RNA amplification process, using RNA
CC derived from the mecA gene as template. Also disclosed is a detection
CC method for a methicillin-resistant S. aureus (MRSA), comprising an RNA
CC amplification process in the presence of a complementary oligonucleotide
CC probe labelled with an intercalated fluorescent dye, where complementary
CC binding of the probe to the RNA transcription product results in a
CC change in the fluorescent property relative to that of a situation where
CC a complex formation is absent, and then measuring the fluorescence
CC intensity of the reaction solution. The oligonucleotides may be used as
CC primers or probes, for detecting methicillin-resistant S. aureus in
CC clinical samples. They may also be used therapeutically to inhibit RNA
CC reverse transcription or translation. These oligonucleotides permit
CC rapid and very sensitive detection/identification of the mecA gene, at a
CC relatively low temperature without the need for heat denaturation of
CC target RNA. The present sequence represents a methicillin resistant
CC Staphylococcus aureus (MRSA) detection oligonucleotide of the invention.
XX
SO Sequence 28 BP; 12 A; 5 C; 3 G; 8 T; 0 other;

Query Match      100.0%; Score 26; DB 24; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAACCTAACTATGATGCTAAAGTTCAAA 28
   |||||||
DB 1 CAACCTAACTATGATGCTAAAGTTCAAA 28

RESULT 2
AAK15487
ID AAK15487 standard; DNA; 108 BP.
XX
AC AAK15487;
XX
DT 07-MAY-1999 (first entry)
XX
DE Probe mecA913-1020 for detecting an antibiotic resistant mecA gene.
XX
KM Antibiotic resistant mecA gene; transmission; treatment:
XX methicillin resistant; Staphylococcus; probe; ss.
XX
S Synthetic.
Staphylococcus sp.
PN
XX MO9901572-A2.
XX
PD 14-JAN-1999.
XX
PF 03-JUL-1998; 98WO-CA00633.
XX
PR 22-JUN-1998; 98US-0090276.
PR 03-JUL-1997; 97US-0051643.
PR 18-MAY-1998; 98US-0086020.
XX
PA (IDH1-) ID H1OMEDICAL CORP.
XX
PI Bekkaoul F, Cloney LP;
XX
DR WP1; 1999-106072/09.
XX
XX Method for determining the presence of an antibiotic resistant mecA
PT gene in a sample - using a scissile link containing nucleic acid
PT probe for antibiotic resistant mecA gene
XX
PS Claim 4; Page 17; 59pp; English.
XX

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```

CC The present sequence represents a probe used for determining the
CC presence of an antibiotic resistant mecA gene in a biological sample.
CC The method provides a means for the rapid detection, for both
CC the prevention of transmission and treatment of, methicillin resistant
CC Staphylococcus species.
XX
SO Sequence 108 BP; 53 A; 14 C; 16 G; 25 T; 0 other;

Query Match      100.0%; Score 28; DB 20; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAACCTAACTATGATGCTAAAGTTCAAA 28
   |||||||
DB 67 CAACCTAACTATGATGCTAAAGTTCAAA 94

RESULT 3
AAT04536
ID AAT04536 standard; cDNA to mRNA; 1789 BP.
XX
AC AAT04536;
XX
DT 11-APR-1996 (first entry)
XX
DE Staphylococcus aureus 'mecA protein coding sequence.
XX
KM methicillin-resistant Staphylococcus aureus; MRSA; 'mecA protein;
XX antibiotic resistance; ds.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT CDS 1..1608
FT /*tag= a
FT /product= 'mec_A-protein
PN
XX JP07209294-A.
XX
PD 11-AUG-1995.
XX
PF 10-JAN-1994; 94JP-(*)2226.
XX
PR 10-JAN-1994; 94JP-0012226.
XX
PA (DENK-) DENKA SEIKEN KK.
PA (KAMA/) KAMANO M.
PA (MTU ) MITSUBISHI CHEM CORP.
XX
DR WP1; 1995-313917/41.
DR P-PSDB; AAR80035.
XX
PT New 'mec A protein and DNA encoding it - used for the detection of
PT methicillin-resistant Staphylococcus aureus
XX
PS Claim 5; Page 11-13; 15pp; Japanese.
XX
XX The present sequence codes for the 'mec A protein which controls
CC methicillin resistance in methicillin-resistant Staph. aureus. The
CC 'mec A protein (mol. wt. 40000) is useful for preparation of
CC antiserum specific for MRSA, thereby allowing methicillin-resistant
CC and methicillin-sensitive strains to be distinguished. The coding
CC sequence was obtained by PCR amplification of the mec A sequence
CC (see AAT04538) using primers AAT04537 and AAT04539.
CC N.B. In the sequence listing of the patent specification, the
CC sequence length is stated to be 1785 bp.
XX
SO Sequence 1789 BP; 735 A; 263 C; 302 G; 489 T; 0 other;

Query Match      100.0%; Score 28; DB 16; Length 1789;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
OY      1 CAACTAATAATGCTGCTAAAGTTCAAA 28
      |||||||
Db      574 CAACTAATAATGCTGCTAAAGTTCAAA 601

RESULT 4
AAQ28599
ID      AAQ28599 standard; DNA; 2007 BP.
XX
XX      AAQ28599;
AC
XX      19-FEB-1993 (first entry)
DT
XX      Encodes penicillin binding protein PBP2A-27R.
DE
XX
XX      Penicillin; antibiotic; bacteria; methicillin; staphylococci;
KW      soluble; chelating peptide; MRS infection; methicillin resistant;
KW      strain.
XX
XX      Staphylococcus aureus strain 27R.
NS
X
FH      Key Location/Qualifiers
FT      CDS 1..2007
FT      /tag= a
XX
XX      PEP505151-A.
PN
XX      23-SEP-1992.
PD
XX
XX      18-MAR-1992; 92EP-0302298.
PR
XX      19-MAR-1991; 91US-0672704.
PR
XX      (ELIL ) LILLY & CO ELI.
PA
XX
XX      Blaszcak IC, Skatrud PL, Smith MC, Wu CYE;
PI      WPI; 1992-318034/39.
DR
XX
XX      Polynucleotide cpd. encoding PBP 2A-27R protein or its deriv. -
PT      contains PBP isolated from staphylococcus aureus and is used to
PT      treat methicillin resistant staphylococci
XX
XX      Disclosure: Page 14; 101pp; English.
PS
XX      This sequence encodes a BBP2A penicillin binding protein isolated
CC      from S. aureus strain 27R. A cDNA library was constructed from
CC      S. aureus DNA in lambda phage EMBL3. Packaging extracts from this
CC      were then used to infect E. coli CJ236. Plaques were screened for the
CC      presence of the mecA-27R gene by a probe produced by PCR amplification
CC      of the mecA gene using primers 028600.1. Positive plaques were purified
CC      and digested with HindIII, and this fragment digested with XbaI and
CC      cloned into M13amp18 and M13amp19 for sequencing.
CC
XX
SO      Sequence 2007 BP; 855 A; 272 C; 341 G; 539 T; 0 other;
Query Match 100.0%; Score 28; DB 13; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 CAACTAATAATGCTGCTAAAGTTCAAA 28
      |||||||
Db      973 CAACTAATAATGCTGCTAAAGTTCAAA 1000

RESULT 5
AA728568
ID      AA728568 standard; DNA; 2007 BP.
XX
XX      AA728568;
AC
XX      01-APR-1997 (first entry)
DT
XX
```

```
DE      Bacterial antibiotic resistance gene, mecA, probe.
XX
XX      Detection; probe; amplification primer; bacterial pathogen; pneumonia;
KW      Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
KW      Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
KW      Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
KW      Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
KW      Haemophilus influenzae; Moraxella catarrhalis; septicemia; meningitis;
KW      infection; intra-abdominal infection; skin infection;
KW      bacterial resistance; beta-lactam antibiotic; ds.
XX
XX      Synthetic.
OS
XX
XX      WO9608582-A2.
PN
XX      21-MAR-1996.
PD
XX
XX      12-SEP-1995; 95WO-CA00528.
PR
XX      12-SEP-1994; 94US-0304732.
PR
XX      (BERG/) BERGERON M.G.
PA      (OUEL/) OUELLETTE M.
PA      (ROY/) ROY P.H.
XX
XX      Bergeron MG, Ouellette M, Roy PH;
PI      WPI; 1996-179953/18.
DR
XX
XX      Method for the detection of bacterial species using probes and
PT      primers - allows detection and quantification of antibiotic
PT      resistant bacteria in patients, the environment and food
XX
XX      Claim 91; Page 144-145; 216pp; English.
PS
XX      The sequences given in AA728568-76 represent fragments derived from
CC      bacterial antibiotic resistance genes which were used as probes in the
CC      method of the invention for the detection of bacterial species in a
CC      sample. The method of the invention comprises using probes and/or
CC      amplification primers which are specific, ubiquitous and sensitive for
CC      determining the presence and/or amount of nucleic acids from selected
CC      bacterial species in any sample, where the bacterial nucleic acid
CC      comprises a selected target region hybridisable with the probes or
CC      primers. The method comprises contacting the sample with the probes
CC      or primers and detecting the presence and/or amount of hybridised
CC      primers or amplification products as and indication of the presence
CC      and/or amount of the bacterial species. This method may be used to
CC      detect commonly encountered bacterial pathogens, e.g. Escherichia coli,
CC      Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis,
CC      Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus
CC      epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus,
CC      Streptococcus pyogenes, Haemophilus influenzae and Moraxella
CC      catarrhalis. These bacterial species are associated with approx. 90% of
CC      urinary tract infections and with a high percentage of other severe
CC      infections, including septicemia, meningitis, pneumonia, intra-abdominal
CC      infections, skin infections and other severe respiratory tract
CC      infections. The method may also be used to evaluate a bacterial
CC      resistance to beta-lactam antibiotics.
CC
XX
SO      Sequence 2007 BP; 855 A; 270 C; 341 G; 541 T; 0 other;
Query Match 100.0%; Score 28; DB 17; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 CAACTAATAATGCTGCTAAAGTTCAAA 28
      |||||||
Db      973 CAACTAATAATGCTGCTAAAGTTCAAA 1000

RESULT 6
AAV68337
ID      AAV68337 standard; DNA; 2007 BP.
```

XX AC AAV68337;
XX XX
DT 21-JUN-1999 (first entry)
XX XX
DE Penicillin binding protein PBP2a meca-27R gene of *S. aureus* 27R.
XX XX
KW Penicillin binding protein; PBP2a-27A; meca-27R gene;
KM methicillin resistance; antibiotic; assay; purification; ss.
XX OS
XX Staphylococcus aureus.
XX PN EP875578-A2.
XX PD 04-NOV-1998.
XX PF 18-MAR-1992: 92EP-0302298.
XX PR 19-MAR-1991: 91US-0672704.
XX (X
XX (ELIL) LILLY & CO EDI.
PI Blaszcak LC, Skatrud PL, Smith MC, Wu CE;
XX DR WPI: 1998-559443/48.
XX DR P-PSDB; AAW81149.
XX XX
XX New Staphylococcus aureus soluble penicillin-binding proteins and
PT their derivatives - useful for screening for compounds effective
PT against methicillin resistant organisms
XX PS Disclosure: Page 14-16; 97pp; English.
XX XX
CC This meca-27R gene encodes penicillin binding protein 2A (PBP2a-27R)
CC responsible for the methicillin resistance of Staphylococcus aureus
CC strain 27R. The invention provides new PBPs of formula SP-L-PBP2As,
CC where: SP is 0 or a signal peptide (preferably from the ampC, ompA or
CC beta-lactamase gene product); L is Met-Val or a compound of formula
CC Met-Gly-CP-(Pro)n-PBP2As, where CP = 0 or a chelating peptide (see
CC AAW81151-56) of formula (His)x(Ai)y-(His)z and A-an amino acid,
CC x=1-10, y=0-4, z=1-10 and monomers, dimers and trimers of above
CC polypeptide where each monomer unit is the same or different; Pro
CC is proline, n = 0 or 1; and PBP2As is soluble PBP2a-27R protein (see
CC AAW81159-62). Also claimed are polynucleotides encoding specific
CC soluble PBP2a compounds. The new PBP2a-27R proteins are useful for
CC assaying for agents useful as antibiotics against methicillin
CC resistant Staphylococcus strains by creating a kinetically inert
CC complex between a support-immobilised transition ion and a modified
CC soluble PBP2a protein comprising a chelating agent, which screens
CC for agents which bind to PBP2a proteins (disclosed). Soluble forms
CC of PBP2a-27R protein facilitate crystallisation as they lack their
CC transmembrane association region, and so are useful for x-ray
CC crystallography studies of the protein, assisting in the design of
CC antibiotic compounds against methicillin resistant Staphylococcus
CC strains (disclosed). The chelating peptide operably linked to the
CC PBP2a-27R proteins is useful for purifying PBPs.
XX SQ Sequence 2007 BP: 855 A; 272 C; 341 G; 539 T; 0 other;
XX
Query Match 100.0%; Score 28; DB 19; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 CAACTAATGATGCTAAAGTTCAA 28
DB 973 CAACTAATGATGCTAAAGTTCAA 1000
RESULT 7
ABN92247
ID ABN92247 standard; DNA; 2007 BP.
XX AC ABA76993;
AC ABA76993;

XX XX
DT 28-JAN-2002 (first entry)
XX XX
DE Antibiotic resistance detection polynucleotide SEQ ID NO 169.
XX XX
KW Detection; bacterial species; animal; food; environment;
KM antibiotic resistance; ds.
XX OS
XX Unidentified.
XX PN NZ501596-A.
XX PD 29-JUN-2001.
XX PF 12-SEP-1995: 95NZ-0501596.
XX PR 12-SEP-1995: 95NZ-0501596.
XX (ID11-) IDI INFECTION DIAGNOSTIC INC.
XX PA Bergeron MC, Ouellette M, Roy PH;
XX PI WPI: 2001-615034/71.
XX DR
XX PT Method for detecting target bacterial species in a sample, comprises
PT detecting the presence or amount of bacterial nucleic acid amplified by
PT a primer derived from bacterial DNA, specific for the target bacterial
PT species -
XX PS Claim 16; Page 159-160; 168pp; English.
XX XX
CC The invention relates to detecting target bacterial species suspected to
CC be present in a sample, comprising contacting nucleic acids of target
CC bacterial species with an amplification primer pair derived from a
CC bacterial DNA fragment (ABA76825-ABA76861) specific for the target
CC bacterial species but ubiquitous for different strains, amplifying the
CC nucleic acid and detecting the presence or amount of an amplified
CC sequence as an indication of the presence or amount of the target
CC bacterial species. The invention includes primers and probes
CC (ABA76862-ABA76984) against the target bacterial species, especially
CC *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *P. mirabilis*, *S. pneumoniae*,
CC *S. aureus*, *S. epidermidis*, *E. faecalis*, *S. saprophyticus*, *S. pyogenes*,
CC *H. influenzae*, *M. catarrhalis* and/or group A Streptococci producing
CC exotoxin A gene spe A, suspected to be present in a sample which is
CC obtained from human patients, animals, environment or food, and which
CC consists of one or more bacterial colonies. Oligonucleotide
CC probes and primers complementary to the bacterial genes encoding
CC resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aacB,
CC aac1, aac2, aac3, aac4, meca, vanA, vanH, vanX, satA, aacA-aphD, vat,
CC vga, msrA, sul and/or int (ABA76985-ABA77001) are also useful to identify
CC commonly encountered and clinically important resistance genes. The
CC invention provides a rapid method of bacterial identification that can be
CC achieved, which reduces the time currently required for the
CC identification of pathogens in the clinical laboratory.
XX SQ Sequence 2007 BP: 855 A; 270 C; 341 G; 541 T; 0 other;
XX
Query Match 100.0%; Score 28; DB 22; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 CAACTAATGATGCTAAAGTTCAA 28
DB 973 CAACTAATGATGCTAAAGTTCAA 1000
RESULT 8
ABN92247
ID ABN92247 standard; DNA; 2028 BP.
XX AC ABN92247;
XX DT 24-JUL-2002 (first entry)


```

XX DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1710.
XX XX
XX KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
XX KW antibacterial; gene therapy; gene; ds.
XX OS Staphylococcus epidermidis.
XX XX
XX PN US6380370-B1.
XX XX
XX PD 30-APR-2002.
XX XX
XX PF 13-AUG-1998; 98US-0134001.
XX XX
XX PR 14-AUG-1997; 97US-055779P.
XX PR 08-NOV-1997; 97US-064964P.
XX XX
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX XX
XX O1 Doucette-Stamm LA, Bush D;
XX X
XX UR MPI; 2002-381255/41.
XX DR P-PSDB: ABP39702.
XX XX
XX PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
XX PT polypeptide, useful for diagnosing and treating bacterial infections -
XX PS
XX PS Disclosure: SEQ ID 1710; 267pp; English.
XX XX
XX CC ARN90538 to ARN93374 represent Staphylococcus epidermidis open reading
XX CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
XX CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
XX CC antibacterial activity and can be used in gene therapy. The sequences
XX CC can also be used in the diagnosis and treatment of bacterial infections,
XX CC particularly S. epidermidis infections. The sequences can be used to
XX CC screen for compounds able to interfere with the S. epidermidis life
XX CC cycle or inhibit S. epidermidis infection.
XX CC N.B. The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from the
XX CC USPTO web site.
XX XX
XX SQ Sequence 2028 BP; 861 A; 273 C; 346 G; 547 T; 1 other;

Query Match 100.0%; Score 28; DB 24; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CACTACTATTGATGCTTAAGTTCAAA 28
   |||||||||||||||||||||||||||
   b 994 CACTACTATTGATGCTTAAGTTCAAA 1021

RESULT 9
AAQ35213
ID AAQ35213 standard; DNA: 2110 BP.
XX XX
XX AC AAQ35213;
XX XX
XX DT 06-JUN-1993 (first entry)
XX XX
XX DE Sequence of the mec A gene.
XX XX
XX KW Methicillin-resistant staphylococci; detection; primer; PCR; ss.
XX XX
XX OS Staphylococcus aureus.
XX XX
XX PH Key location/Qualifiers
XX FT CDS 105..2110
XX FT /*tag= a
XX PN EP527628-A.
XX PD 17-FEB-1993.

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XX XX
XX PF 10-AUG-1992; 92EP-0307307.
XX XX
XX PR 13-AUG-1991; 91US-0744770.
XX XX
XX PA (BLIL ) LILLY & CO ELI.
XX XX
XX PI Skatrud PL, Unal S;
XX XX
XX DR MPI; 1993-054352/07.
XX DR P-PSDB: AAR30845.
XX XX
XX PT Detection of methicillin-resistant staphylococci - using
XX PT polymerase chain reaction method, and DNA primers, for rapid,
XX PT sensitive and accurate detection
XX XX
XX PS Disclosure: Pages 7-10; 16pp; English.
XX XX
XX CC The inventors claim a method for detecting methicillin-resistant
XX CC staphylococcal infections which involves the use of the PCR primed
XX CC by fragments of the Staphylococcus meca gene. More specifically, the
XX CC initial primers used are nucleotides 141-160 and the inverse
XX CC complement of nucleotides 1929-1952 of the S. aureus meca gene. The
XX CC interior primers are nucleotides 568-593 and the inverse complement
XX CC of 1647-1670 of the S. aureus meca gene.
XX XX
XX SQ Sequence 2110 BP; 896 A; 290 C; 350 G; 574 T; 0 other;

Query Match 100.0%; Score 28; DB 14; Length 2110;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CACTACTATTGATGCTTAAGTTCAAA 28
   |||||||||||||||||||||||||||
   Db 1077 CACTACTATTGATGCTTAAGTTCAAA 1104

RESULT 10
AAQ25905
ID AAQ25905 standard; DNA: 2322 BP.
XX XX
XX AC AAQ25905;
XX XX
XX DT 18-JAN-1993 (first entry)
XX DE PB2'.
XX XX
XX KW Polymerase chain reaction; PCR; amplification; ss.
XX XX
XX OS Synthetic.
XX XX
XX FH Key location/Qualifiers
XX FT misc_binding 1581..1598
XX FT /*tag= a
XX FT /label= Probe_binding_site
XX XX
XX PN JP04169200-A.
XX XX
XX PD 17-JUN-1992.
XX XX
XX PF 31-OCT-1990; 90JP-0296708.
XX PF 31-OCT-1990; 90JP-0296708.
XX PR 31-OCT-1990; 90JP-0296708.
XX XX
XX PA (SHIO ) SHIONOGI & CO LTD.
XX XX
XX DR MPI; 1992-253403/31.
XX XX
XX PT Detection of PB2' gene for determn. of methicillin-resistance -
XX PT useful esp. for detection of methicillin-resistance
XX PT Staphylococcus aureus
XX PS Disclosure: Fig 1; 9pp; Japanese.

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```
XX The sequence given is the PBP2' gene. This gene could be detected
CC by the primer sequences given in AA025897-904. Due to the results of
CC this amplification reaction resistance to methicillin in Staphylococcus
CC aureus could be determined.
XX
SQ Sequence 2322 BP: 940 A; 324 C; 389 G; 669 T; 0 other:
Query Match 100.0%; Score 28; DB 13; Length 2322;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CAACCTACTATTGATGCTAAAGTTCAA 28
Db 979 CAACCTACTATTGATGCTAAAGTTCAA 1006
|||||
RESULT 11
AA04538
ID AA04538 standard; cDNA to mRNA: 2455 BP.
X
X AA04538;
AX 11-APR-1996 (first entry)
DT
XX Staphylococcus aureus mecA protein coding sequence.
DE
XX methicillin-resistant Staphylococcus aureus; MRSA; 'meca' protein;
KW antibiotic resistance; ds.
OS Staphylococcus aureus.
XX
XX Key location/Qualifiers
FH 134..2146
FT /*tag= a
TT /product= mec_A-protein
FN
PN JP07209294-A.
XX
XX 11-AUG-1995.
PD
XX 10-JAN-1994; 94JP-00122226.
PF
XX 10-JAN-1994; 94JP-00122226.
PR
XX 10-JAN-1994; 94JP-00122226.
XX
XX (DENK-) DENKA SEIKEN KK.
PA (KAWA-) KAWANO M.
PA (MITU) MITSUBISHI CHEM CORP.
XX
X WPI: 1995-313917/41.
X P-PSDB: AAR80036.
XX
XX New 'mec A' protein and DNA encoding it - used for the detection of
PT methicillin-resistant Staphylococcus aureus
PT
PS Example 2; Page 8-10; 15pp; Japanese.
XX
XX The present sequence codes for the mec A protein. DNA coding for
CC the 'mec A' protein, which controls methicillin resistance in
CC methicillin-resistant Staph. aureus (MRSA), was obtained by PCR
CC amplification of the mec A sequence using primers AA04537 and
CC AA04539. The 'mec A' protein (mol. wt. 40000) is useful for
CC preparation of antiserum specific for MRSA, thereby allowing
CC methicillin-resistant and methicillin-sensitive strains to be
CC distinguished.
XX
XX Sequence 2455 BP: 997 A; 344 C; 401 G; 713 T; 0 other:
Query Match 100.0%; Score 28; DB 16; Length 2455;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CAACCTACTATTGATGCTAAAGTTCAA 28
```

```
DB 1112 CAACCTACTATTGATGCTAAAGTTCAA 1139
|||||
RESULT 12
AAH01187
ID AAH01187 standard; DNA: 2456 BP.
XX
XX AAH01187;
XX
XX 24-JUL-2001 (first entry)
DT
XX
XX Staphylococcus aureus nucleotide sequence SEQ ID NO:1178.
DE
XX Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitica;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial;
KW vaccine; primer; ds.
XX
XX Staphylococcus aureus.
OS
XX
XX MO200123604-A2.
PN
XX 05-APR-2001.
PD
XX 28-SEP-2000; 2000WO-CA01150.
PP
XX 28-SEP-1999; 99CA-2283458.
PR 19-MAY-2000; 2000CA-2307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
PA
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Placard FJ, Roy PH;
XX WPI: 2001-24506/25.
XX
XX Nucleic acid sequences are used to generate universal probes and
PT primers which can be used to identify and detect the presence of algal,
PT archaeal, bacterial, fungal and parasitica species in a test sample -
XX
XX Disclosure: Page 1048-1049; 1580pp; English.
XX
XX The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitica
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal
CC and parasitica species, genus, family and group. A nucleic acid (I)
CC obtained using the method of the invention can be used for the universal
CC detection of any bacterium, fungus or parasite in a sample and for the
CC detection of at least one antimicrobial agent resistance gene or at
CC least one toxin gene. hexa nucleic acids are used for the specific and
CC ubiquitous detection and for identification of Streptococcus pneumoniae.
CC (I) can be used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp.,
CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC provides faster results than substrate specificity tests as results can
CC be determined in an hour and improved accuracy is also achieved.
CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
CC which are given in the exemplification of the present invention.
XX
XX Sequence 2456 BP: 1001 A; 344 C; 396 G; 715 T; 0 other:
```



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XX 31-OCT-1996; 96US-0029960.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M;
XX Kunsch CA, Rosen CA;
XX WPI: 1998-272225/24.
XX
XX Computer-readable medium with recorded Streptococcus pneumoniae
XX polynucleotide sequences - useful in diagnostic kits and assays, and
XX pharmaceutical compositions and vaccines for Streptococcus
XX pneumoniae
XX
XX Claim 1: Page 332-339; 1409pp; English.
XX
XX The present invention describes a computer readable medium which has
XX the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)
XX recorded on it, or a representative fragment or a sequence at least 95%
XX identical to SEQ ID NO:1 to 391. The nucleotide sequences depicted in
XX SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
XX Streptococcus pneumoniae. The present invention also describes an
XX isolated nucleic acid molecule encoding a homologue of any of the
XX fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the
XX nucleic acid molecule is produced by a process comprising: (a) screening
XX a genomic DNA library using as a probe a target sequence defined by any
XX of the sequences in SEQ ID NO:1 to 391, identifying members of the
XX library which contain sequences that hybridise to the target sequence and
XX isolating the nucleic acid molecules from the members; or (b) isolating
XX mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid
XX molecules whose nucleotide sequence is homologous to amplification
XX primers derived from the fragment of the S. pneumoniae genome to prime
XX the amplification and isolating the amplified sequences. The computer
XX readable medium can be used in a computer-based system for identifying
XX fragments of the S. pneumoniae genome of commercial importance, or
XX expression modulating fragments of the S. pneumoniae genome. Products
XX from the present invention can be used in diagnosis kits and assays, and
XX pharmaceutical compositions and vaccines for S. pneumoniae.
XX
SQ Sequence 13206 BP; 4016 A; 2929 C; 2473 G; 3786 T; 2 other;
Query Match 73.6%; Score 20.6; DB 19; Length 13206;
Best Local Similarity 85.2%; Pred. No. 40;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 AACTACTATTGATGCTAAAGTTCAA 28
  777 AACTACTATTGATGCTAAAGTTCA 751

```

Search completed: December 10, 2002, 17:32:46
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 20:17:24 : Search time 36.2905 Seconds
(without alignments)
300.853 Million cell updates/sec

Title: US-09-865-579A-25

Perfect score: 28

Sequence: 1 caactaactatgtatgctaaagttcaaa 28

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Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

otal number of hits satisfying chosen parameters: 700850

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published_Applications_MA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	US-09-865-579A-25	Sequence 25, Appl
2	28	100.0	2007	US-09-452-599-169	Sequence 169, App
3	19.2	68.6	491	US-09-560-863-992	Sequence 992, App
4	18.2	65.0	475	US-10-062-254-359	Sequence 359, App
5	18	64.3	462	US-09-770-444-398	Sequence 398, App
6	18	64.3	3645	US-09-815-242-4853	Sequence 4853, App
7	18	64.3	3807	US-09-815-242-9015	Sequence 9015, App
8	18	64.3	7067	US-09-764-877-3222	Sequence 3222, App
9	18	64.3	7311	US-09-815-242-4779	Sequence 4779, App
10	18	64.3	18846	US-09-815-242-8898	Sequence 8898, App
11	17.6	62.9	466	US-09-880-107-1287	Sequence 1287, App
12	17.6	62.9	510	US-09-777-364-1720	Sequence 1720, App
13	17.6	62.9	551	US-09-920-300A-290	Sequence 290, App
14	17.6	62.9	551	US-10-033-528-290	Sequence 290, App
15	17.6	62.9	585	US-09-962-436-3	Sequence 3, Appl
16	17.6	62.9	1500	US-09-842-552-83	Sequence 83, Appl
17	17.6	62.9	1737	US-09-815-242-8403	Sequence 8403, App
18	17.6	62.9	6176	US-09-823-109-6	Sequence 6, Appl
19	17.6	62.9	640681	US-09-790-988-1	Sequence 1, Appl

c	20	17.4	62.1	1482	10	US-09-070-927A-842	Sequence 842, App
c	21	17.4	62.1	3212	10	US-09-070-927A-428	Sequence 428, App
c	22	17.4	62.1	174493	10	US-09-804-471A-3	Sequence 3, Appl
c	23	17.4	62.1	462	10	US-09-287-070-3	Sequence 3, Appl
c	24	17.4	62.1	508	10	US-09-287-070-10	Sequence 10, Appl
c	25	17.4	62.1	843	10	US-09-938-842A-2426	Sequence 2426, App
c	26	17.4	62.1	1311	10	US-09-815-242-7057	Sequence 7057, App
c	27	17.4	62.1	1359	9	US-09-938-842A-1312	Sequence 1312, App
c	28	17.4	62.1	1889	10	US-09-287-070-4	Sequence 4, Appl
c	29	17.4	62.1	1936	10	US-09-954-456-1138	Sequence 1138, App
c	30	17.4	62.1	5530	10	US-09-070-927A-206	Sequence 206, App
c	31	16.8	60.0	405	9	US-10-046-935-1092	Sequence 1092, App
c	32	16.8	60.0	405	9	US-09-878-178-1092	Sequence 1092, App
c	33	16.8	60.0	485	10	US-09-922-217-505	Sequence 505, App
c	34	16.8	60.0	485	10	US-09-833-263-505	Sequence 505, App
c	35	16.8	60.0	486	10	US-09-070-927A-744	Sequence 744, App
c	36	16.8	60.0	1268	10	US-09-070-927A-401	Sequence 401, App
c	37	16.8	60.0	2000	9	US-09-938-842A-3175	Sequence 3175, App
c	38	16.8	60.0	2000	9	US-09-938-842A-4603	Sequence 4603, App
c	39	16.8	60.0	2388	10	US-09-815-242-7124	Sequence 7124, App
c	40	16.8	60.0	2435	10	US-09-823-038A-40	Sequence 40, Appl
c	41	16.8	60.0	143068	10	US-09-967-768A-316	Sequence 316, App
c	42	16.6	59.3	258	10	US-09-923-876-1148	Sequence 1148, App
c	43	16.6	59.3	2000	9	US-09-938-842A-3189	Sequence 3189, App
c	44	16.6	59.3	2000	9	US-09-938-842A-3326	Sequence 3326, App
c	45	16.6	59.3	2132	12	US-10-044-090-659	Sequence 659, App

ALIGNMENTS

RESULT 1
US-09-865-579A-25
Sequence 25, Application US/09865579A
Patent No. US20020098492A1
GENERAL INFORMATION:
APPLICANT: Taya, Toshiki
APPLICANT: Ishiguro, Takahiko
TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
FILE REFERENCE: 9558-003-27
CURRENT APPLICATION NUMBER: US/09/865, 579A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: JP 2000-163149
PRIOR FILING DATE: 2000-05-29
PRIOR APPLICATION NUMBER: JP 2000-179394
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-865-579A-25
Query Match 100.0%, Score 28; DB 10; length 28;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 CAACCTACTATTCATCTAAAGTTCAAA 28
1 CAACCTACTATTCATCTAAAGTTCAAA 28
RESULT 2
US-09-452-599-169
Sequence 169, Application US/09452599
Patent No. US20020055101A1
GENERAL INFORMATION:
APPLICANT: Bergeron, Michel G.

```
; APPLICANT: Ouclette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patenlin Ver. 2.1
; LENGTH: 2007
; SEQ ID NO 169
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169
```

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Query Match 100.0%; Score 28; DB 10; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CAACTAAGTATTGATGCTAAAGTCAAA 28
DB 973 CAACTAAGTATTGATGCTAAAGTCAAA 1000
```

```
RESULT 3
US-09-560-863-992
; Sequence 992, Application US/09560863
; Patent No. US20020110809A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael C.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020110809A1el Human Polynucleotides and the
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: LEX-0018-USA
; CURRENT APPLICATION NUMBER: US/09/560,863
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/132,408
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 992
; LENGTH: 491
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(491)
; OTHER INFORMATION: n = A,T,C or G
US-09-560-863-992
```

```
Query Match 68.6%; Score 19.2; DB 10; Length 491;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
OY 4 CTAACTATTGATGCTAAAGTTCAA 27
DB 296 CTAACTTTGCTGCTAAAGTTCAA 319
```

```
RESULT 4
US-10-062-254-359
; Sequence 359, Application US/10062254
; Patent No. US20020138882A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B
; APPLICANT: Cahoon, Rebecca E
```

```
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Pang, Yiwen
; APPLICANT: Hanke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved in Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 359
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
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; NAME/KEY: unsure
; LOCATION: (36)
; NAME/KEY: unsure
; LOCATION: (285)
; NAME/KEY: unsure
; LOCATION: (298)
; NAME/KEY: unsure
; LOCATION: (368)
; NAME/KEY: unsure
; LOCATION: (440)
; NAME/KEY: unsure
; LOCATION: (463)
; NAME/KEY: unsure
; LOCATION: (475)
US-10-062-254-359
```

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Query Match 65.0%; Score 18.2; DB 12; Length 475;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```
OY 2 AACTAAGTATTGATGCTAAAGTTC 25
DB 429 AACTAAGTATTGATGCTAAAGTTC 452
```

```
RESULT 5
US-09-770-444-398/c
; Sequence 398, Application US/09770444
; Patent No. US2002023280A1
```

```

: GENERAL INFORMATION:
: APPLICANT: Gorlach, Jörn
: APPLICANT: An, Yong-Qiang
: APPLICANT: Hamilton, Carol M.
: APPLICANT: Price, Jennifer L.
: APPLICANT: Raines, Tracy M.
: APPLICANT: Yu, Yang
: APPLICANT: Rameaka, Joshua G.
: APPLICANT: Hage, Amy
: APPLICANT: Mathew, Abraham V.
: APPLICANT: Ledford, Brooke L.
: APPLICANT: Woessner, Jeffrey P.
: APPLICANT: Haas, William David
: APPLICANT: Garcia, Carlos A.
: APPLICANT: Kricker, Maja
: APPLICANT: Stader, Fred
: APPLICANT: Davis, Keith R.
: APPLICANT: Allen, Keith
: APPLICANT: Hoffman, Neil
: APPLICANT: Hurban, Patrick
: TITLE OF INVENTION: Expressed Sequences of Arabidopsis
: FILE REFERENCE: 2027 (PARA-016PRV)
: CURRENT APPLICATION NUMBER: US/09/770,444
: PRIOR FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/178,502
: NUMBER OF SEQ ID NOS: 999
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 398
: LENGTH: 462
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
: US-09-770-444-398

Query Match          64.3%: Score 18: DB 10: Length 462:
Best Local Similarity 80.8%: Pred. No. 80:
Matches 21: Conservative 0: Mismatches 5: Indels 0: Gaps 0:

QY 3 ACTAAGTATTGATGCTAAAGTTCAAA 28
Db 139 ACTAAGTATTGATGCTAATTTCAGA 114

RESULT 6
US-09-815-242-4853
: Sequence 4853, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Karl L.
: APPLICANT: zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: TITLE OF INVENTION: Prokaryotes
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: PRIOR FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
```

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: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4853
: LENGTH: 3645
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
: US-09-815-242-4853

Query Match          64.3%: Score 18: DB 10: Length 3645:
Best Local Similarity 80.8%: Pred. No. 1e+02:
Matches 21: Conservative 0: Mismatches 5: Indels 0: Gaps 0:

QY 3 ACTAAGTATTGATGCTAAAGTTCAAA 28
Db 771 ACAAGCTATTATGATATAAGCTCAA 796

RESULT 7
US-09-815-242-9015
: Sequence 9015, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Karl L.
: APPLICANT: zyskind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: TITLE OF INVENTION: Prokaryotes
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: PRIOR FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9015
: LENGTH: 3807
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(3807)
: US-09-815-242-9015

Query Match          64.3%: Score 18: DB 10: Length 3807:
Best Local Similarity 80.8%: Pred. No. 1e+02:
Matches 21: Conservative 0: Mismatches 5: Indels 0: Gaps 0:

QY 3 ACTAAGTATTGATGCTAAAGTTCAAA 28
Db 933 ACAAGCTATTATGATATAAGCTCAA 958

RESULT 8
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US-09-764-877-3222/c
; Sequence 3222, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3222
; LENGTH: 7067
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3222

Query Match      64.3%; Score 18; DB 10; Length 7067;
Best Local Similarity 80.8%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY      3 ACTACTATGCTGCTTAAGTTCAA 28
      ||| ||||| ||| ||| ||||| |||
Db      5626 ACTTACTATGAGAGCTTAAGTTCAA 5601

RESULT 9
US-09-815-242-4779
; Sequence 4779, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4779
; LENGTH: 7311
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4779

Query Match      64.3%; Score 18; DB 10; Length 7311;
Best Local Similarity 80.8%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY      3 ACTACTATGCTGCTTAAGTTCAA 28
      ||| ||||| ||| ||| ||||| |||
Db      11799 ACAAGCTATTATGATGAAGCTCAA 11824

RESULT 10
US-09-815-242-8898
; Sequence 8898, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8898
; LENGTH: 18846
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(18846)
US-09-815-242-8898

Query Match      64.3%; Score 18; DB 10; Length 18846;
Best Local Similarity 80.8%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY      3 ACTAAGCTATTGATGCTTAAGTTCAA 28
      ||| ||||| ||| ||| ||||| |||
Db      11799 ACAAGCTATTATGATGAAGCTCAA 11824

RESULT 11
US-09-880-107-1287
; Sequence 1287, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
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SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1287
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA476754
US-09-880-107-1287

Query Match          62.9%; Score 17.6; DB 10; Length 466;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 TAACTATGATGCTAAAGTCAA 28
DB 303 TAGCTATTGAGCTTAAGCTGCAA 326

RESULT 12
US-09-777-564-1720/c
Sequence 1720, Application US/09777564
; Patent No. US20020022591A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.493
; CURRENT APPLICATION NUMBER: US/09/777,564
; CURRENT FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 1730
; SOFTWARE: FASTSEQ for Window Version 4.0
; SEQ ID NO 1720
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-777-564-1720

Query Match          62.9%; Score 17.6; DB 10; Length 510;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 AACTAATGATGCTAAAGTTC 25
DB 203 AACTGACTTCTGATCATTAAGTTC 180

RESULT 13
US-09-920-300A-290
Sequence 290, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 290
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-290

Query Match          62.9%; Score 17.6; DB 10; Length 551;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```
OY 2 AACTAATGATGCTAAAGTTC 25
DB 490 AACTGACTTCTGATCATTAAGTTC 513

RESULT 14
US-10-033-528-290
Sequence 290, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 290
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-290

Query Match          62.9%; Score 17.6; DB 12; Length 551;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 AACTAATGATGCTAAAGTTC 25
DB 490 AACTGACTTCTGATCATTAAGTTC 513

RESULT 15
US-09-962-436-3/c
Sequence 3, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using SI
; TITLE OF INVENTION: Sels
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or c
US-09-962-436-3

Query Match          62.9%; Score 17.6; DB 10; Length 585;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 TAACTATGATGCTAAAGTCAA 28
DB 298 TAGCTATTGAGCTTAAGCTGCAA 275

Search completed: December 11, 2002, 06:14:07
Job time : 42.2905 secs
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OM nucleic - nucleic search, using sw model

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(without alignments)
224.980 Million cell updates/sec

Title: US-09-865-579A-25

Perfect score: 28

Sequence: 1 caactaactatgctgaagtcacaa 28

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Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/1/1na/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/1na/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/1na/PCrus.COMB.seq:*
6: /cgn2_6/ptodata/1/1na/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	2007	2	US-08-743-637B-169
2	28	100.0	2007	3	US-08-526-840B-169
3	28	100.0	2028	4	US-09-134-001C-1710
4	20.6	73.6	13206	4	US-08-961-527-33
5	20.6	73.6	16995	4	US-08-961-527-82
6	19	67.9	2996	4	US-08-961-527-260
7	19	67.9	11309	4	US-08-961-527-108
8	18.6	66.4	226	4	US-09-235-451-40
9	18.6	66.4	11443	4	US-08-961-527-49
10	17.8	63.6	3946	4	US-09-453-702B-103
11	17.4	62.1	548	4	US-08-642-274D-21
12	17.4	62.1	548	4	US-08-952-014C-21
13	17.4	62.1	851	4	US-08-961-527-361
14	17.4	62.1	1074	4	US-08-961-527-382
15	17.4	62.1	2714	3	US-09-002-298-4
16	17.4	62.1	4398	4	US-08-961-527-293
17	17.4	62.1	8898	4	US-08-961-527-69
18	17.4	62.1	38564	4	US-09-734-673-3
19	17	60.7	2495	4	US-08-961-527-255
20	17	60.7	4290	4	US-08-961-527-255
21	17	60.7	11887	4	US-08-924-629C-4
22	16.8	60.0	998	4	US-08-961-527-146
23	16.8	60.0	2667	4	US-09-227-357-62
24	16.8	60.0	5183	1	US-08-134-001C-195
25	16.8	60.0	5183	2	US-08-459-568-3
26	16.8	60.0	5868	3	US-08-399-411-3
27	16.8	60.0	5868	4	US-08-516-859A-3
					US-09-586-472-3

28	16.8	60.0	5868	4	US-09-528-706-3	Sequence 3, Appli
29	16.8	60.0	72604	4	US-09-268-992-7	Sequence 7, Appli
30	16.8	60.0	72604	4	US-09-657-474-7	Sequence 7, Appli
31	16.6	59.3	741	4	US-09-134-001C-2455	Sequence 2455, Ap
32	16.6	59.3	1599	1	US-08-143-219-27	Sequence 27, Appli
33	16.6	59.3	8648	4	US-09-415-946-2	Sequence 2, Appli
34	16.6	59.3	17341	4	US-09-415-946-1	Sequence 1, Appli
35	16.6	59.3	31880	4	US-09-453-702B-242	Sequence 242, App
36	16.4	58.6	453	4	US-09-134-001C-881	Sequence 881, App
37	16.4	58.6	562	4	US-09-328-111-468	Sequence 468, App
38	16.4	58.6	903	4	US-09-134-001C-1620	Sequence 1620, Ap
39	16.4	58.6	2167	3	US-08-961-083-83	Sequence 83, Appli
40	16.4	58.6	2810	4	US-09-105-390-6	Sequence 6, Appli
41	16.4	58.6	2884	1	US-08-148-209A-5	Sequence 5, Appli
42	16.4	58.6	14735	4	US-08-961-527-171	Sequence 171, App
43	16.4	58.6	15363	4	US-08-961-527-139	Sequence 139, App
44	16.4	58.6	19702	4	US-08-961-527-7	Sequence 7, Appli
45	16.4	58.6	51259	3	US-08-781-891-209	Sequence 209, App

ALIGNMENTS

RESULT 1
US-08-743-637B-169
Sequence 169, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGRON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/743.637B
APPLICATION NUMBER: US/08/743.637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526.840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414)277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0% Score 28; DB 2; Length 2007;

Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CAACTAATTGATGCTAAAGTTCAAA 28
DB 973 CAACTAATTGATGCTAAAGTTCAAA 1000

RESULT 2

US-08-526-840B-169
Sequence 169, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: APPLICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586,90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAACTAATTGATGCTAAAGTTCAAA 28
DB 973 CAACTAATTGATGCTAAAGTTCAAA 1000

RESULT 3

US-09-134-001C-1710
Sequence 1710, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucelle-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: CTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1710
LENGTH: 2028
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
FEATURE:
NAME/KEY: unsure
LOCATION: (52)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 28; DB 4; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAACTAATTGATGCTAAAGTTCAAA 28
DB 994 CAACTAATTGATGCTAAAGTTCAAA 1021

RESULT 4

US-08-961-527-33/C
Sequence 33, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 13206 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-33

Query Match 73.6%; Score 20.6; DB 4; Length 13206;
Best Local Similarity 85.2%; Pred. No. 3.6;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTACTATTGATGCTAAAGTTCAA 28
||||||| ||||| ||||| ||||| |||||
Db 777 AACTACTATTGATGATAAAGTTCAGA 751

RESULT 5

US-08-961-527-82/C
Sequence 82, Application US/08961527
Patent No. 6420135

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences

NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,527

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB340P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 82:

SEQUENCE CHARACTERISTICS:

LENGTH: 1695 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-961-527-82

Query Match 73.6%; Score 20.6; DB 4; Length 1695;
Best local similarity 85.2%; Pred. No. 3.6;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTACTATTGATGCTAAAGTTCAA 28
||||||| ||||| ||||| ||||| |||||
Db 456 AACTACTATTGATGATAAAGTTCAGA 430

RESULT 6

US-08-961-527-260

Sequence 260, Application US/08961527

Patent No. 6420135

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences

NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,527

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB340P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 260:

SEQUENCE CHARACTERISTICS:

LENGTH: 2996 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-961-527-260

Query Match 67.9%; Score 19; DB 4; Length 2996;
Best local similarity 81.5%; Pred. No. 15;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACTACTATTGATGCTAAAGTTCAA 28
||||||| ||||| ||||| ||||| |||||
Db 2181 AACTACTATTGATGATAAAGTTCAGA 2207

RESULT 7

US-08-961-527-108/C

Sequence 108, Application US/08961527

Patent No. 6420135

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences

NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,527

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB340P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:

LENGTH: 11309 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

```

; TOPOLOGY: linear
US-08-961-527-108
Query Match
Best Local Similarity 67.9%; Score 19; DB 4; Length 11309;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACTACTATTGATGCTAAAGTTCA 28
   ||||| ||||| ||||| |||||
DB 9189 AATTACTTATGATGATTAAGTTCCACA 9163

RESULT 8
US-09-235-451-40
; Sequence 40, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Blake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 40
; LENGTH: 226
; TYPE: DNA
; ORGANISM: R. rattus
US-09-235-451-40

Query Match
Best Local Similarity 66.4%; Score 18.6; DB 4; Length 226;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACTACTATTGATGCTAAAGTTTC 25
   ||||| ||||| ||||| |||||
DB 70 CAAGTACTCTGATGCTGAAGTTTC 94

RESULT 9
US-08-961-527-49
; Sequence 49, Application US/08961527
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44b storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11443 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-49

Query Match
Best Local Similarity 66.4%; Score 18.6; DB 4; Length 11443;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTACTATTGATGCTAAAGTTCA 26
   ||||| ||||| ||||| |||||
DB 10721 AATTACTTATGATGATTAAGTTCA 10745

RESULT 10
US-09-453-702B-103/c
; Sequence 103, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Bialtner, Frederick R.
; APPLICANT: Perna, Nicole T.
; APPLICANT: Plunkett, Guy
; TITLE OF INVENTION: No. 6365723e1 Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-DEC-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296,95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3946
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-09-453-702B-103

Query Match
63.6%; Score 17.8; DB 4; Length 3946;
```

Best Local Similarity 90.5%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AACTACTATGATGCTAAAG 22
|||||
DB 3539 AACTACTGTCGATGTTAAAG 3519

RESULT 11

US-08-642-274D-21
; Sequence 21, Application US/08642274D
; Patent No. 6200749
; GENERAL INFORMATION:
; APPLICANT: Shiloh, Yosef
; TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO
; FILE REFERENCE: 229000033
; CURRENT APPLICATION NUMBER: US/08/642,274D
; CURRENT FILING DATE: 1996-05-03
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 21
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: genomic
US-08-642-274D-21

Query Match 62.1%; Score 17.4; DB 4; Length 548;
Best Local Similarity 77.8%; Pred. No. 61;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 AACTACTATGATGCTAAAGTCAAA 28
|||||
DB 206 ACCTAAACATGATGTTAAAGTTTAA 232

RESULT 12

US-08-952-014C-21
; Sequence 21, Application US/08952014C
; Patent No. 6265158
; GENERAL INFORMATION:
; APPLICANT: Shiloh, Yosef
; TITLE OF INVENTION: ATAXIA-TELANGIECTASIA GENE AND ITS
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6265158thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,014C
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I
; REGISTRATION NUMBER: 30,995
; REFERENCE/DOCKET NUMBER: 2290,00028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 810-539-5050
; TELEFAX: 810-539-5055
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 548 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-952-014C-21

Query Match 62.1%; Score 17.4; DB 4; Length 548;
Best Local Similarity 77.8%; Pred. No. 61;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 AACTACTATGATGCTAAAGTCAAA 28
|||||
DB 206 ACCTAAACATGATGTTAAAGTTTAA 232

RESULT 13

US-08-961-527-361
; Sequence 361, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SPD ID NO: 361:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 851 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-361

Query Match 62.1%; Score 17.4; DB 4; Length 851;
Best Local Similarity 77.8%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 AACTACTATGATGCTAAAGTCAAA 28
|||||
DB 6 AATTAGTTATGATGATTAAGTTCAGA 32

RESULT 14

US-09-134-001C-382
; Sequence 382, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

```

: TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: GTC-007
: CURRENT APPLICATION NUMBER: US/09/134,001C
: PRIOR FILING DATE: 1998-08-13
: PRIOR APPLICATION NUMBER: US 60/064,964
: PRIOR FILING DATE: 1997-11-08
: PRIOR APPLICATION NUMBER: US 60/055,779
: NUMBER OF SEQ ID NOS: 5674
: SEQ ID NO 382
: LENGTH: 1074
: TYPE: DNA
: ORGANISM: Staphylococcus epidermidis
: US-09-134-001C-382

```

```

Query Match      62.1%; Score 17.4; DB 4; Length 1074;
Best Local Similarity 77.8%; Pred. No. 64;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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```

Oy      2  AACTACTATTGATGCTAAAGTTCAAA 28
          ||||| ||||| || ||| |||||
          , 671 AACTAAATATTGTGTGAAGATGAAA 697

```

```

RESUL.T 15
US-09-002-298-4
: Sequence 4, Application US/09002298
: Patent No. 6046001
: GENERAL INFORMATION:
: APPLICANT: Handman, Olga
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Guegler, Karl J.
: APPLICANT: Corley, Neil C.
: APPLICANT: Tang, Y. Tom
: APPLICANT: Shah, Purvi
: TITLE OF INVENTION: HUMAN FATTY ACID BETA-OXIDATION ENZYMES
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Dr.
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/002,298
: FILING DATE: Filed Herewith
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-845-4166
: TELEFAX: 650-855-0555
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2714 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: OVARUT02
: CLONE: 2595635
: US-09-002-298-4

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Query Match      62.1%; Score 17.4; DB 3; Length 2714;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy      2  AACTACTATTGATGCTAAAGTTCAAA 28
          ||||| ||||| ||||| ||||| |||||
          Db 1945 AACTGACTGTCTGCTAAAGACACAAA 1971

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Search completed: December 10, 2002, 22:54:57
Job time : 48.2926 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 17:08:34 ; Search time 1435.66 Seconds
(without alignments)
315.863 Million cell updates/sec

Title: US-09-865-579A-25

Perfect score: 28

Sequence: 1 caactaactatgctgctaaagtctcaaa 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
otal number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estcl:*
10: gb_estcl2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estlmu:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	21.6	77.1	471	12	BF611176
2	21.6	77.1	497	12	BG160008
3	21.6	77.1	505	13	BJ041404
4	21.6	77.1	511	13	BJ059576
5	21.6	77.1	512	13	BJ060237
6	21.6	77.1	727	13	BK398481

7	20.6	73.6	504	17	AQ876537
8	20.6	73.6	638 <td>13</td> <td>BJ073806</td>	13	BJ073806
9	20	71.4	268 <td>17</td> <td>CNS000KW</td>	17	CNS000KW
10	20	71.4	394 <td>17</td> <td>BH366114</td>	17	BH366114
11	20	71.4	479 <td>17</td> <td>AL759527</td>	17	AL759527
12	20	71.4	548 <td>17</td> <td>CNS00P03</td>	17	CNS00P03
13	20	71.4	574	17	BH742194
14	20	71.4	621	17	BH275516
15	20	71.4	809	13	BM397184
16	20	71.4	986	13	BM397185
17	19.8	70.7	568	17	BH204118
18	19.8	70.7	817	17	BH590452
19	19.8	70.7	908	17	BH159183
20	19.6	70.0	427	9	AU228638
21	19.6	70.0	524	14	BM878732
22	19.6	70.0	603	13	BJ046096
23	19.6	70.0	631	17	AQ964844
24	19.6	70.0	637	17	A2641775
25	19.6	70.0	652	17	AQ964845
26	19.6	70.0	654	17	A2522960
27	19.6	70.0	704	13	BJ055250
28	19.2	68.6	149	9	AL175727
29	19.2	68.6	309	9	AL175723
30	19.2	68.6	376	10	AM614066
31	19.2	68.6	409	10	AM590962
32	19.2	68.6	418	10	BE549830
33	19.2	68.6	422	12	BG150398
34	19.2	68.6	427	9	AI825501
35	19.2	68.6	436	17	B45942
36	19.2	68.6	439	10	AM241919
37	19.2	68.6	450	10	BE671743
38	19.2	68.6	451	10	AM136189
39	19.2	68.6	453	9	AA996869
40	19.2	68.6	454	12	BF059501
41	19.2	68.6	466	12	BG150455
42	19.2	68.6	463	10	AV757278
43	19	67.9	287	10	BA473037
44	19	67.9	323	13	BI073600
45	19	67.9	324	14	Z18129

ALIGNMENTS

RESULT 1
BF611176 471 bp mRNA linear EST 14-DEC-2000
LOCUS dd76b03.y1 Wellcome CRC pcDNA1 egg Xenopus laevis cDNA clone
DEFINITION IMAGE:3430204 5', mRNA sequence.
ACCESSION BF611176
VERSION
KEYWORDS
SOURCE
ORGANISM African clawed frog.
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodidae; Xenopus.
1 (bases 1 to 471)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,
B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
Washu Xenopus EST project, 1999
Unpublished (1999)
Other-ESTs: dd76b03.x2
Contact: Sandy Clifton, Ph.D.
Washu Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estevatson.wustl.edu
Library constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B.


```

VERSION      BJ059576.1 GI:17492916
KEYWORDS     EST.
SOURCE       African clawed frog.
ORGANISM     Xenopus laevis
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
              Xenopodinae; Xenopus.
REFERENCE    1 (bases 1 to 511)
AUTHORS      Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
              ,Y.
TITLE        Expressed genes in X. laevis embryo
JOURNAL      Unpublished (2001)
COMMENT      Contact: Tadasu Shin-i
              Center For Genetic Resource Information
              National Institute of Genetics
              1111 Yata, Mishima, Shizuoka 411-8540, Japan
              Tel: 81-559-81-6856
              Fax: 81-559-81-6855
              Email: tshin@genes.nig.ac.jp.
              Location/Qualifiers
                1..511
                /organism="Xenopus laevis"
                /db_xref="taxon:8355"
                /clone_lib="X1063a03"
                /clone_lib="NIBB Mochii normalized Xenopus tailbud
                library"
                /tissue_type="whole embryo"
                /dev_stage="stage 25"
                /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
                were oligo-dT primed and directionally cloned. Staging
                according to Nieuwkoop and Faber. Library is subtracted
                and was constructed by N. Garrett and A.M. Zorn,
                (Wellcome/CRC Institute)."
BASE COUNT   143 a      104 c      98 g      165 t      1 others
ORIGIN
Query Match  77.1%; Score 21.6; DB 13; Length 511;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACTAAGTATTGATGCTAAAGTTCAA 28
    |||||  || ||||| ||||| |||||
Db 285 CAGCTAATTATGATGCTAAAGTGCAAA 312

RESULT 5
LOCUS      BJ060237 512 bp mRNA linear EST 11-DEC-2001
DEFINITION laevis cDNA clone X1065d05 5', mRNA sequence.
ACCESSION  BJ060237
VERSION     BJ060237.1 GI:17496967
KEYWORDS   EST.
SOURCE     African clawed frog.
ORGANISM   Xenopus laevis
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
              Xenopodinae; Xenopus.
REFERENCE    1 (bases 1 to 512)
AUTHORS      Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
              ,Y.
TITLE        Expressed genes in X. laevis embryo
JOURNAL      Unpublished (2001)
COMMENT      Contact: Tadasu Shin-i
              Center For Genetic Resource Information
              National Institute of Genetics
              1111 Yata, Mishima, Shizuoka 411-8540, Japan
              Tel: 81-559-81-6856
              Fax: 81-559-81-6855
              Email: tshin@genes.nig.ac.jp.
              Location/Qualifiers
                1..512
                /organism="Xenopus laevis"

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```

                /db_xref="taxon:8355"
                /clone_lib="X1065d05"
                /clone_lib="NIBB Mochii normalized Xenopus tailbud
                library"
                /tissue_type="whole embryo"
                /dev_stage="stage 25"
                /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
                were oligo-dT primed and directionally cloned. Staging
                according to Nieuwkoop and Faber. Library is subtracted
                and was constructed by N. Garrett and A.M. Zorn,
                (Wellcome/CRC Institute)."
BASE COUNT   145 a      101 c      101 g      164 t      1 others
ORIGIN
Query Match  77.1%; Score 21.6; DB 13; Length 512;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACTAAGTATTGATGCTAAAGTTCAA 28
    |||||  || ||||| ||||| |||||
Db 267 CAGCTAATTATGATGCTAAAGTGCAAA 294

RESULT 6
LOCUS      BM398481 727 bp mRNA linear EST 17-JAN-2002
DEFINITION Tetrahymena thermophila cDNA (large fraction)
ACCESSION  BM398481
VERSION     BM398481.1 GI:18198534
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila.
              Tetrahymena thermophila.
              Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
              Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE    1 (bases 1 to 727)
AUTHORS      Turkewitz,A.P., Karreer,K.M., Jahn,C., Ortas,E., Kirk,K.E., Frankel
              ,J. and Klobuchar,L.
TITLE        EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
              Molecular Genetics and Cell Biology
              University of Chicago
              920 E. 58th Street, Chicago, IL 60637, USA
              Tel: 773 702 4374
              Fax: 773 702 3172
              Email: apturkew@midway.uchicago.edu
              Seq primer: 73.
              Location/Qualifiers
                1..727
                /organism="Tetrahymena thermophila"
                /strain="CU428.1"
                /db_xref="taxon:5911"
                /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                /note="Vector: Bluescript2 SK+; Details on library
                preparation can be found in Chilcoat and Turkewitz (2001)
                Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT   260 a      94 c      141 g      232 t
ORIGIN
Query Match  77.1%; Score 21.6; DB 13; Length 727;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAACTAAGTATTGATGCTAAAGTTCAA 28
    |||||  || ||||| ||||| |||||
Db 216 CAACTAATTCGTGATGCTCAATTTCAAA 189

RESULT 7
LOCUS      A0876537 504 bp DNA linear GSS 09-NOV-1999
DEFINITION HS_2001_B2_G05_MR CIT Approved Human Genomic Sperm Library D Homo

```

ACCESSION	sapientis genomic clone Plate=2001 Col=10 Row=N, DNA sequence.			
VERSION	A0876537			
KEYWORDS	A0876537.1 GI:6308004			
SOURCE	GSS.			
ORGANISM	human.			
REFERENCE	Homo sapiens			
AUTHORS	EuroKyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 504)			
TITLE	Mahiras.G.G., Wallace.J.C., Smith.K., Swartzell.S., Holzman.T., Keller.A., Shaker.R., Furlong.J., Young.J., Zhao.S., Adams.M.D. and Hood.L.			
JOURNAL MEDLINE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome			
COMMENT	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589			
	Contact: Mahiras GG, Wallace JC, Hood L			
	High Throughput Sequencing Center			
	401 Queen Anne Avenue North, Seattle, WA 98109, USA			
	Tel: (206) 616-3618			
	Fax: (206) 616-3687			
	Email: jwallace@u.washington.edu			
	Clones may be purchased from Research Genetics (info@resgen.com).			
	BAC end Web Server: http://www.htsc.washington.edu			
	Plate: 2001 row: N column: 10			
	Seq primer: M13 Reverse			
	Class: BAC ends			
FEATURES	High quality sequence stop: 504.			
source	Location/Qualifiers			
	1..504			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="Plate=2001 Col=10 Row=N"			
	/clone.lib="CIT Approved Human Genomic Sperm Library D"			
	/sex="male"			
	/note="Organ: sperm; Vector: phebDACL1; BAC Clones in E-Coli DH10B"			
BASE COUNT	115 a	139 c	78 g	158 t
ORIGIN	14 others			
Query Match	73.6%; Score 20.6; DB 17; Length 504;			
Best Local Similarity	85.2%; Pred.No.1.7e+02;			
Matches	23; Conservative	0; Mismatches	4; Indels	0; Caps
0Y	1 CAACCTACACTGATGCTAAATCTCA 27			
Db	257 CAACCTACCTTTGATCGCTTACGACAA 283			
LOCUS	B073806 638 bp mRNA linear EST 11-DEC-2001			
DEFINITION	B073806 NIBB Mochi normalized Xenopus tailbud library Xenopus laevis cDNA clone Xl.101e02 5', mRNA sequence.			
ACCESSION	B073806			
VERSION	B073806.1 GI:17503995			
KEYWORDS	EST.			
SOURCE	African Clawed Frog.			
ORGANISM	Xenopus laevis			
REFERENCE	EuroKyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus. 1 (bases 1 to 638)			
AUTHORS	Kikayama.A., Terasaka.C., Mochi.M., Ueno.N., Shin-I.T. and Kohara.Y.			
TITLE	Expressed genes in X. laevis embryo			
JOURNAL	unpublished (2001)			
COMMENT	Contact: Tadasu Shin-i			
	Center For Genetic Resource Information			
	National Institute of Genetics			
	1111 Yata, Mishima, Shizuoka 411-8540, Japan			
	Tel: 81-559-81-6856			

FEATURES	Source	1. 638	/organism="Xenopus laevis"	
		/db_xref="taxon:8355"		
		/clone="X1101602"		
		/clone_lib="NIBB Mochii normalized Xenopus tailbud library"		
		/tissue_type="whole embryo"		
		/dev_stage="stage 25"		
		/note="vector: pBSRN3; Site.1: NotI; Site.2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is substracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."		
BASE COUNT	158 a	145 c	160 g	175 t
ORIGIN				
Query Match	73.6%	Score 20.6;	DB 13;	Length 638;
Best Local Similarity	83.2%	Fred. No. 1.9e+02;		
Matches	23;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0.
OY	1	CACCTAAGTATGATGCTAAAGTTCAA	27	
DB	612	CAGCTAATTAAATGATGCTAAAGTTCAA	638	
RESULT 9				
CNS000KM/c				
LOCUS	CNS000KM	268 bp	DNA	linear
DEFINITION	Arabidopsis thaliana genome survey sequence sp6 end of HAC P11K19 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.			
ACCESSION	AL085934			
VERSION	AL085934.1	GI:5287074		
KEYWORDS	GSS.			
ORGANISM	Arabidopsis thaliana.			
SOURCE	Arabidopsis thaliana			
	Eurayotla; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.			
REFERENCE	1 (bases 1 to 268)			
AUTHORS	Salanoubat,M., Choise,N., Artiguenave,F., Brottier,P., Wincker,P., Samson,D., Saurin,W., Weissenbach,J. and Queller,F.			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 268)			
AUTHORS	Genoscope.			
TITLE	Direct Submission			
JOURNAL	Submitted (23-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrel@genoscope.cns.fr			
FEATURES	- Web : www.genoscope.cns.fr			
Source	Location/Qualifiers			
	1. .268			
	/organism="Arabidopsis thaliana"			
	/strain="Columbia"			
	/db_xref="taxon:3702"			
	/clone="F11K19"			
	/clone_lib="IGF"			
	/note="end : SP6"			
BASE COUNT	75 a	70 c	54 g	69 t
ORIGIN				
Query Match	71.4%	Score 20;	DB 17;	Length 268;
Best Local Similarity	82.1%	Fred. No. 2.4e+02;		
Matches	23;	Conservative	0;	Mismatches 5; Indels 0; Gaps 0.
OY	1	CACCTAAGTATGATGCTAAAGTTCAA	28	
DB	215	CACCTAAGCTTGTGACGCTAAGTTCAA	188	
RESULT 10				

BH366114 394 bp DNA linear CSS 03-DEC-2001
 LOCUS CH230-75F8.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
 DEFINITION CH230-75F8, DNA sequence.
 ACCESSION BH366114
 VERSION BH366114.1 GI:17296848
 KEYWORDS CSS.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 394)
 Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shwartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
 Rat BAC End Sequences from Library CHORI-230 EcoRI segment
 Unpublished (1999)
 Other GSSs: CH230-75F8.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library availability, please contact Pieter de Jong (pdejong@email.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
 Plate: 75 row: F column: 8
 Seq primer: SP6
 Class: BAC ends.
 Location/Qualifiers
 1..394
 /organism="Rattus norvegicus"
 /strain="BN/SSNHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-75F8"
 /clone_lib="CHORI-230 Segment 1"
 /sex="female"
 /cell_type="Brain"
 /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by Pieter de Jong"
 BASE COUNT 137 a 81 c 66 g 110 t
 ORIGIN

Query Match 71.4%; Score 20; DB 17; Length 394;
 Best Local Similarity 82.1%; Pred. No. 2.8e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 CAACCTAATGATGCTAAAGTCAAA 28
 ||||| ||||| ||||| ||||| |||||
 Db 92 CAACCAACTACTAATCTAATAATTCAA 119

RESULT 11
 LOCUS AL759527/c 479 bp DNA linear CSS 18-JUN-2002
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-188A08-014624,
 genomic survey sequence.
 ACCESSION AL759527
 VERSION AL759527.1 GI:21497875
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids 1; Brassicales; Brassicaceae; Arabidopsids.
 REFERENCE 1

AUTHORS Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
 and Weissshaar,B.
 TITLE A pipeline for automated high-throughput generation of ESTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transformed lines
 JOURNAL Unpublished
 REFERENCE 2
 AUTHORS Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weissshaar,B.
 TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics
 JOURNAL Unpublished
 REFERENCE 3
 AUTHORS Li,Y., Rosso,M., Strizhov,N. and Weissshaar,B.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer
 Zuechlingsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion close to or within gene At3g47850. The
 sequences are generated at the MPI for plant Breeding Research in
 the context of the GABI-Kat project. GABI-Kat is part of the German
 Plant Genomics program designated 'GABI'. Information on line
 availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
 Location/Qualifiers
 1..479
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-188A08-014624"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161. The lines contain one or more T-DNA
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"
 BASE COUNT 150 a 109 c 111 g 109 t
 ORIGIN

Query Match 71.4%; Score 20; DB 17; Length 479;
 Best Local Similarity 82.1%; Pred. No. 3e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 CAACCTAATGATGCTAAAGTCAAA 28
 ||||| ||||| ||||| ||||| |||||
 Db 358 CAACCTACGCTTGACCTCAAGCTTCAAA 331

RESULT 12
 LOCUS CNS00P03/c 548 bp DNA linear CSS 28-JUN-1999
 DEFINITION Arabidopsis thaliana genome survey sequence T7 end of BAC F7M17 of
 IGF library from strain Columbia of Arabidopsis thaliana, genomic
 survey sequence.
 ACCESSION AL083889
 VERSION AL083889.1 GI:5285029
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids 1; Brassicales; Brassicaceae; Arabidopsids.
 REFERENCE 1 (bases 1 to 548)
 AUTHORS Salanoubat,M., Choisme,N., Artiguenave,F., Brottier,P., Wincker,P.,
 Samson,D., Saurin,W., Weissenbach,J. and Queller,F.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 548)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY ccdex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr

FEATURES
 Location/Qualifiers
 1..548
 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="F7M17"
 /clone_lib="TGF"
 /note="end : T7"

BASE COUNT
 160 a 109 c 137 g 142 t

ORIGIN
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 Best Local Similarity 82.1% Pred. No. 3.2e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
 ||||| 1 ||||| 1111 111111
 Db 205 CAACTCACTCTTGCACCTTAAGTTCAAA 178

RESULT 13
 BH742194 574 bp DNA linear GSS 25-FEB-2002
 LOCUS g143b05.g1 Bobuds01 Brassica oleracea genomic clone g143b05 5', DNA
 DEFINITION sequence.
 ACCESSION BH742194
 VERSION BH742194.1 GI:18876807
 KEYWORDS GSS.
 SOURCE Brassica oleracea.
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 574)
 Katar, M., O'Shaughnessy, A., Palmer, L., Bahret, A., Baker, J., Balija
 V., Cunniff, D.M., Katzenberger, P., King, L., Kirchoff, K., Kuit, K.,
 Miller, B., Muller, S., Nascimento, L., Preston, R., Santos, L., Shah, R.,
 Zutavern, T., Dedha, N., Radniewicz, P.D. and McCombie, W.R.
 Whole Genome Shotgun Reads from Brassica oleracea (2002b)
 Unpublished (2002)
 Contact: W. Richard McCombie
 Cold Spring Harbor Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Plate: g143 row: b column: 05
 Seq primer: -210n1Rev
 Class: shotgun
 High quality sequence stop: 574.
 Location/Qualifiers
 1..574
 /organism="Brassica oleracea"
 /db_xref="taxon:3712"
 /clone="g143b05"
 /clone_lib="Bobuds01"
 /note="Vector: M13 for .x reads, pBluescript for .b and .g
 reads; Site_1: EcoRV; Whole genome shotgun library from
 flowering buds. DNA was purified from a crude nuclear prep
 using Brassica oleracea TO1000DH3 buds provided by Thomas
 Osborn at the University of Wisconsin. Genomic DNA
 provided by Pablo Radniewicz (CSHL) and shotgun library
 prepared in McCombie lab."

BASE COUNT
 216 a 91 c 80 g 187 t

ORIGIN
 Query Match 71.4% Score 20; DB 17; Length 574;
 Best Local Similarity 82.1% Pred. No. 3.2e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
 | 1 11 1111 1111 11111111
 Db 539 CCAATATATTATTAATGCTTAAGTTCAAA 566

RESULT 14
 BH275516 621 bp DNA linear GSS 30-NOV-2001
 LOCUS BH275516
 DEFINITION CH230-83N9.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
 CH230-83N9, DNA sequence.
 ACCESSION BH275516
 VERSION BH275516.1 GI:17187918
 KEYWORDS GSS.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 621)
 Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn
 A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
 Jong, P. and Fraser, C.M.
 Rat BAC End Sequences from Library CHORI-230 EcORI segment
 Other_GSSs: CH230-83N9.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@email.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering/information.htm). BAC end
 page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
 Plate: 83 row: N column: 9
 Seq primer: SP6
 Class: BAC ends.
 Location/Qualifiers
 1..621
 /organism="Rattus norvegicus"
 /strain="BN/SNHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-83N9"
 /clone_lib="CHORI-230 Segment 1"
 /sex="Female"
 /cell_type="Brain"
 /note="Vector: PTARPA2.1; Site_1: EcoRI; Site_2: EcoRI;
 CHORI-230 Rat (BN/SNHsd/MCW) BAC library produced by
 Pieter de Jong"

BASE COUNT
 199 a 131 c 118 g 173 t

ORIGIN
 Query Match 71.4% Score 20; DB 17; Length 621;
 Best Local Similarity 82.1% Pred. No. 3.3e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
 |||| 1111 1 11 1111 111111
 Db 154 CACAAACTACTAATACTAAATTCAAA 181

RESULT 15
 BM397184/c 809 bp mRNA linear EST 17-JAN-2002
 LOCUS BM397184
 DEFINITION 5009-0-3-A09.t.1 Chilcoal/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM397184
 VERSION BM397184.1 GI:18197237
 KEYWORDS EST.

SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 REFERENCE 1 (bases 1 to 809)
 AUTHORS Turkewitz,A.P., Karer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
 ,J. and Klobulcher,L.
 TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: 73.
 FEATURES Location/Qualifiers
 source 1..809
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 BASE COUNT 312 a 87 c 156 g 254 t
 ORIGIN
 Query Match 71.4%; Score 20; DB 13; Length 809;
 Best Local Similarity 82.1%; Pred. No. 3.7e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CAACTAATCTATGATGCTAAAGTTCAA 28
 ||||| | ||||| | | |||||
 DB 192 CAACTAATCTGATGCTCAATTCAA 165

Search completed: December 10, 2002, 22:50:18
 Job time : 1439.66 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2002, 16:38:09 ; Search time 607.084 Seconds

(without alignments)
1342.283 Million cell updates/sec

Title: US-09-865-579A-25

Perfect score: 28

Sequence: 1 caactactatgtatgctaagttcaaa 28

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapexl 1.0

Searched: 2054640 seqs, 14551402878 residues

otal number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBml:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vt:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	AX306866	AX306866 Sequence
2	28	100.0	1789	E09772	E09772 The base se
3	28	100.0	2007	AR089410	AR089410 Sequence
4	28	100.0	2007	AR093610	AR093610 Sequence
5	28	100.0	2322	SABBP	YU0688 Staphylococ
6	28	100.0	2322	E03736	E03736 DNA sequenc
7	28	100.0	2454	SEMECAPB	X52592 S. epidermi
8	28	100.0	2455	E09771	E09771 The base se
9	28	100.0	2456	SAEMECAPB	X52593 S. aureus m
10	28	100.0	2456	AX110445	AX110445 Sequence
11	28	100.0	5596	SSK8MECA	Y13096 S. sciuri me
12	28	100.0	6368	SSK3MECA2	Y13095 S. sciuri me
13	28	100.0	9047	SAMECAR11	Y14051 Staphylococ
14	28	100.0	21777	AB063173	AB063173 Staphyloc
15	28	100.0	26090	AB063172	AB063172 Staphyloc
16	28	100.0	39332	AB033763	AB033763 Staphyloc
17	28	100.0	58237	DB6934	DB6934 Staphylococ
18	28	100.0	68256	AB037671	AB037671 Staphyloc
19	28	100.0	290250	AP004822	AP004822 Staphyloc
20	28	100.0	298050	AP003129	AP003129 Staphyloc
21	28	100.0	349999	AP003358	AP003358 Staphyloc
22	22.2	79.3	5806	SSK3MECA1	Y13052 S. sciuri me
23	22.2	79.3	349980	AX417038	AX417038 Sequence
24	22.2	79.3	349980	AX417041	AX417041 Sequence
25	21.2	75.7	11608	AF125160	AF125160 Rattus no
26	21.2	75.7	192419	AC110094	AC110094 Rattus no
27	20.6	73.6	247	BLCO11	X90409 B. lucorum D
28	20.6	73.6	5068	SSK1MECA	Y09223 S. sciuri me
29	20.6	73.6	6684	SSK1MECA	Y13094 S. sciuri me
30	20.6	73.6	8592	AE010503	AE010503 Fusobacte
31	20.6	73.6	10029	AE007351	AE007351 Streptoco
32	20.6	73.6	11692	AE007454	AE007454 Streptoco
33	20.6	73.6	13206	BD003713	BD003713 Polynucle
34	20.6	73.6	16995	BD003762	BD003762 Polynucle
35	20.6	73.6	120492	CXY43W8C	AI032637 Caenorhab
36	20.6	73.6	163820	AC123878	AC123878 Mus muscu
37	20.6	73.6	178521	AC126450	AC126450 Mus muscu
38	20.6	73.6	232807	SPNEU1901	AL449923 Streptoco
39	20.6	73.6	248254	SPNEU1903	AL449925 Streptoco
40	20.2	72.1	186766	AL732294	AL732294 Mus muscu
41	20.2	72.1	245087	AC091606	AC091606 Mus muscu
42	20	71.4	969	AY116964	AY116964 Arabidops
43	20	71.4	1107	AF436027	AF436027 Neotrypae
44	20	71.4	1160	AF428310	AF428310 Arabidops
45	20	71.4	1168	AY086386	AY086386 Arabidops

ALIGNMENTS

RESULT 1
AX306866
LOCUS AX306866 28 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 25 from Patent Epl160333.
ACCESSION AX306866
VERSION AX306866.1 GI:17894688
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequences.
REFERENCE
1
Tava, T., Ishiguro, T. and Saito, J.
Oligonucleotides and method for detection of meca gene of
methicillin-resistant Staphylococcus aureus
Patent: EP 1160333-A 25 05-DEC-2001;
JOURNAL

Pred. No. is the number of results predicted by chance to have a

FEATURES Tosoh Corporation (JP)
Location/Qualifiers
1..28
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 12 a 5 c 3 g 8 t

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 CACTAAGTATGATGCTAAAGTTCAAA 28
|||||
Db 1 CACTAAGTATGATGCTAAAGTTCAAA 28

RESULT 2
E09772 1789 bp RNA linear PAT 29-SEP-1997
LOCUS The base sequence of modified meca DNA.
ACCESSION E09772
VERSION E09772.1 GI:22026401
KEYWORDS JP 1995209294-A/2.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 1789)
AUTHORS Kono, M., Hiramatsu, K., Sasazu, M., Noguchi, M. and Suguro, K.
TITLE NOVEL 'MECA PROTEIN' CODING DNA THEREFOR, AND DETECTION METHOD FOR METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
JOURNAL Patent: JP 1995209294-A 2 11-AUG-1995;
KONO MEGUMI, MITSUBISHI CHM CORP, DENKA SEIKEN CO LTD
COMMENT OS Staphylococcus aureus
PN JP 1995209294-A/2
PD 11-AUG-1995
PF 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI MASAHISA,
PI SUGURO KAZUYA
PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC C12R1:19),
PC (C12P21/02,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH key Location/Qualifiers
FT source 1..1789
FT /organism="Staphylococcus aureus" FT CDS
FEATURES 1..1789
Location/Qualifiers
source /product="Modified meca".
BASE COUNT 735 a 263 c 302 g 489 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 1789;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CACTAAGTATGATGCTAAAGTTCAAA 28
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Db 574 CACTAAGTATGATGCTAAAGTTCAAA 601

RESULT 3
AR089410 2007 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 169 from patent US 5994066.
DEFINITION
ACCESSION AR089410

VERSION AR089410.1 GI:10016167
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2007)
AUTHORS Bergeron, M.G., Picard, F.J., Ouellette, M. and Roy, P.H.
TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 5994066-A 169 30-NOV-1999;
FEATURES Location/Qualifiers
source 1..2007
BASE COUNT 855 a 270 c 341 g 541 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CACTAAGTATGATGCTAAAGTTCAAA 28
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Db 973 CACTAAGTATGATGCTAAAGTTCAAA 1000

RESULT 4
AR093610 2007 bp DNA linear PAT 08-SEP-2000
LOCUS Sequence 169 from patent U. 6001564.
DEFINITION AR093610
ACCESSION AR093610
VERSION AR093610.1 GI:10020359
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2007)
AUTHORS Bergeron, M.G., Ouellette, M. and Roy, P.H.
TITLE Species specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 6001564-A 169 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..2007
BASE COUNT 855 a 270 c 341 g 541 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CACTAAGTATGATGCTAAAGTTCAAA 28
|||||
Db 973 CACTAAGTATGATGCTAAAGTTCAAA 1000

RESULT 5
SABP 2322 bp DNA linear BCT 12-SEP-1993
LOCUS Staphylococcus aureus (MRSA) PBP gene for beta-lactam-inducible penicillin-binding protein.
ACCESSION Y00688
VERSION Y00688.1 GI:46628
KEYWORDS penicillin-binding protein.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 2322)
AUTHORS Song, M.D., Wach, M., Dol, M., Ishino, F. and Matsubashi, M.
TITLE Evolution of an inducible penicillin-target protein in

methicillin-resistant *Staphylococcus aureus* by gene fusion
 JOURNAL FEBS Lett. 221 (1), 167-171 (1987)
 MEDLINE 87304805
 PUBMED 3305073
 REFERENCE 2 (bases 1 to 2322)
 AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
 Harberis-Maino, L., Kayser, F. H. and Berger-Bachi, B.
 Sequence comparison of meca genes isolated from
 methicillin-resistant *Staphylococcus aureus* and *Staphylococcus*
epidermidis
 JOURNAL Gene 94 (1), 137-138 (1990)
 MEDLINE 91033056
 PUBMED 2227446
 COMMENT Data kindly reviewed (13.1.88) by Matsubashi.
 FEATURES
 source
 1..2322
 Location/Qualifiers
 /organism="Staphylococcus aureus"
 /db_xref="taxon:1280"
 1..2013
 /note="penicillin-binding protein (AA 1-670)"
 /codon_start=1
 /transl_table=11
 /protein_id="CAA68684.1"
 /db_xref="GI:46629"
 /db_xref="SWISS-PROT:P07944"
 /translation="MKKIKYPLIILVVVVGCGIYFVASKDKKINNTIDAIEDKNFKQ
 VYKDSYISKSDNGEVEEMTERPIKIVNSGVINDIRIKKVSNNKRRVDAQYKIK
 TNYGINDRVOENFEKEDGMKLDHSDYIIGOMKDSIHLENKSEKGIIDRNNY
 ELANGTHMRIGLIPKVNKSKDYKAIKAKLEISDYINKKAKIIPSPHFRTVK
 KMDYISDPAKKFFLTNTETESRNPICAKTSHLGYGPIINSEBELKQKYEYGRDAA
 VIKKGLKELYDKLOHEDGKRVTVI VRVDNSNTIAHTLIERKKKDGKDIQLTIDKAV
 OKSIYNNKNDVSGSTAIHPOTGELLALVSTPSYDVPYPMGMSNEEYKMLTEDKKEP
 LNKFOITTSPTSGSTKILAMIGLNKTLIDDTSYKIDGKQKDSMGCVAVTREV
 VNGNIDLKQAISSSNIFEKALGSLGSKFEKMGKLGVEDIPSDYFPYVAQISNK
 NIDNELLDASGGGGEILINVOILISTYSALENNGINAPHLKDTKMKWKNKITS
 KENINLLNGMOGVYKTHKEDIRSYALIGKSGTAEIKMGQFGRCQIGCFISYDK
 DNPNNMAINVDYODKCMASINAKISGVYDELVEYENGKKYDIDE"

BASE COUNT 940 a 324 c 369 g 669 t
 ORIGIN

Query Match 100.0%; Score 28; DB 1; Length 2322;
 Best Local Similarity 100.0%; Pred. No. 0.94;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTACTATGATGCTAAAGTTCAA 28
 |||||||||||||||||||||||||||||
 Db 979 CAACTACTATGATGCTAAAGTTCAA 1006

RESULT 6
 LOCUS E03736 2322 bp DNA linear PART 29-SEP-1997
 DEFINITION DNA sequence of PBP2' gene for determination of methicillin
 resistance.
 E03736
 VERSION E03736.1 GI:2171951
 KEYWORDS JP 1992169200-A/9.
 SOURCE unidentified.
 ORGANISM unidentified
 unclassified.
 1 (bases 1 to 2322)
 REFERENCE 1 (bases 1 to 2322)
 AUTHORS Watanabe, Y., Nakamura, E., Teraoka, H., Wada, K., Minamide, W. and
 Murakami, K.
 DETECTION OF PBP 2' GENE AND JUDGEMENT OF METHICILLIN RESISTANCE
 Patent: JP 1992169200-A 9 17-JUN-1992;
 SHIONOGI & CO LTD
 OS (methicillin resistant) *staphylococcus aureus*
 PN JP 1992169200-A/9
 PD 17-JUN-1992
 PE 31-OCT-1990 JP 1990296708
 PI WATANABE YUKIHIKO, NAKAMURA ETSUO, TERAOKA HIROSHI, WADA KOJI,
 MINAMIDE WAKIO, MURAKAMI KAZUHIISA
 PC C1201/68.C12N15/11;

CC strandedness: Single;
 CC topology: linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH Key Location/Qualifiers
 FT misc_feature 1..2322
 /note="PBP2' gene for determination of
 methicillin resistance"
 FT Location/Qualifiers
 1..2322
 /organism="unidentified"
 /db_xref="taxon:332644"

BASE COUNT 939 a 324 c 390 g 669 t
 ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 2322;
 Best Local Similarity 100.0%; Pred. No. 0.94;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTACTATGATGCTAAAGTTCAA 28
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 Db 979 CAACTACTATGATGCTAAAGTTCAA 1006

RESULT 7
 LOCUS SEMECAPB 2454 bp DNA linear BCT 12-SEP-1993
 DEFINITION S. epidermidis meca gene for PBP2' (penicillin binding protein 2').
 ACCESSION X52592.1 GI:46993
 VERSION X52592.1
 KEYWORDS meca gene; methicillin resistance; penicillin-binding protein 2'.
 SOURCE *Staphylococcus epidermidis*.
 ORGANISM *Staphylococcus epidermidis*.
 bacteria: Firmicutes; Bacillales; *Staphylococcus*.
 REFERENCE 1 (bases 1 to 2454)
 AUTHORS Ryffel, C.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
 Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
 REFERENCE 2 (bases 1 to 2454)
 AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
 Barberis-Maino, L., Kayser, F. H. and Berger-Bachi, B.
 Sequence comparison of meca genes from methicillin-resistant
Staphylococcus aureus and *Staphylococcus epidermidis*
 Gene (1990) In press
 JOURNAL 3 (bases 1 to 2454)
 REFERENCE 3 (bases 1 to 2454)
 AUTHORS Ryffel, C.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUL-1990) Ryffel C., University of Zuerich, Inst of
 Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
 REFERENCE 4 (bases 1 to 2454)
 AUTHORS Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P. E.,
 Barberis-Maino, L., Kayser, F. H. and Berger-Bachi, B.
 Sequence comparison of meca genes isolated from
 methicillin-resistant *Staphylococcus aureus* and *Staphylococcus*
epidermidis
 JOURNAL Gene 94 (1), 137-138 (1990)
 MEDLINE 91033056
 PUBMED 2227446
 COMMENT See also <X52593-4> and <Y00688>.
 Data kindly reviewed (23-JUL-1990) by C. Ryffel.
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 /strain="WT55"
 /db_xref="taxon:1282"
 /clone="WT80/WT79"
 80..85
 /note="-35 region"
 101..105
 promoter
 promoter
 promoter

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          /note="ribosome binding site"
precursor_RNA 141..2159
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CDS       141..2147
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ELANTGAEVIGIYPRKNSKKDYKAIKEISIDFIKQOMDMVDDPVPPLKTYK
KMDHYISDFKKRHLTTNETESRNTPLGKATSHLGVCFINSELKOKYKCKQDA
VIGRKGLEKLYDKRLOHEDGVRVIVDNSNTIAHTLIEKKRDKDQIQLTDAKVOK
SIYNNMNDYSGSTAIHPOTGELLALVSTPSYDVPPMGSMNEYNKLTDEKKEPLL
NKFOITSTPGSTOKILTYMIGLNNKTLIDKTSYKIDGKQDKSMGCVNTRYEVN
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BASE COUNT 997 a 345 c 398 g 714 t
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Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTCAAA 28
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Db 1113 CAACTAACTATTGATGCTAAAGTCAAA 1140

RESULT 8
LOCUS      E09771 2455 bp RNA linear PAT 29-SEP-1997
DEFINITION The base sequence of meca DNA.
ACCESSION  E09771
VERSION     E09771.1 GI:22026400
KEYWORDS   JP 1995209294-A/1.
SOURCE     Staphylococcus aureus.
ORGANISM   Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE  1 (bases 1 to 2455)
AUTHORS   Kono, M., Hiramatsu, K., Sasazu, M., Noguchi, M. and Suguro, K.
TITLES    NOVEL 'MECA PROTEIN, CODING DNA THEREFOR, AND DETECTION METHOD FOR
METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
Patent: JP 1995209294-A 1 11-AUG-1995;
JOURNAL    KONO MEGUMI, MITSUBISHI CHEM CORP, DENKA SEIKEN CO LTD
OS Staphylococcus aureus
PN JP 1995209294-A/1
PD 11-AUG-1995
PF 10-JAN-1994 JP 1994012226
PI KONO MEGUMI, HIRAMATSU KEIICHI, SASAZU MITSUNORI, PI NOGUCHI
MASAHISA,

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PI SUGURO KAZUYA
PC G01N33/53,C07K14/31,C12N1/21,C12N15/09,C12P21/02,C12N1/21, PC
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PC (C12P21/02,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..2455
FT 134..2146 /organism="Staphylococcus aureus" FT CDS
FT /product="meca protein".
FEATURES
source Location/Qualifiers
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/db_xref="taxon:1280"
BASE COUNT 997 a 344 c 401 g 713 t
ORIGIN
Query Match      100.0%; Score 28; DB 6; Length 2455;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTCAAA 28
|||||
Db 1112 CAACTAACTATTGATGCTAAAGTCAAA 1139

RESULT 9
LOCUS      SAMECAPB 2456 bp DNA linear BCT 12-SEP-1993
DEFINITION S. aureus meca gene for PBP2' (penicillin binding protein 2').
ACCESSION  X52593
VERSION     X52593.1 GI:46610
KEYWORDS   meca gene: methicillin resistance; penicillin-binding protein;
penicillin-binding protein 2.
SOURCE     Staphylococcus aureus.
ORGANISM   Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE  1 (bases 1 to 2456)
AUTHORS   Ryffel, C.
TITLES    Direct Submission
JOURNAL    Submitted (05-APR-1990) Ryffel C., University of Zuerich, Inst of
Medical Microbiology, Gloriastr 32, CH-8028 Zuerich, Switzerland
REFERENCE  2 (bases 1 to 2456)
AUTHORS   Ryffel, C., Tesch, W., Birch-Machin, I., Reynolds, P.E.,
Barberis-Maino, L., Kayser, F.H. and Berger-Bachli, B.
TITLES    Sequence comparison of meca genes isolated from
methicillin-resistant Staphylococcus aureus and Staphylococcus
epidermidis
JOURNAL    Gene 94 (1), 137-138 (1990)
MEDLINE    91033056
PUBMED    2227446
COMMENT    See also <X52592>, <X52594> and <Y00688>.
Data kindly reviewed (23-JUL-1990) by C. Ryffel.
FEATURES
source Location/Qualifiers
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101..105
/note="10 region"
130..134
/note="ribosome binding site"
141..2153
/note="primary transcript"
141..2147
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2702..2707
RBS
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BASE COUNT 1991 a 856 c 821 g 1928 t
ORIGIN
Query Match 100.0%; Score 28; DB 1; Length 5596;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAACTAATTTGATGCTAAAGTTCAA 28
Db 3685 CAACTAATTTGATGCTAAAGTTCAA 3712
RESULT 12
SSK3MECA2
LOCUS SSK3MECA2 6368 bp DNA linear BCT 16-JAN-1998

DEFINITION S. sciuri meca2 gene, strain K3 (MM2).
ACCESSION Y13095
VERSION Y13095.1 GI:2791912
KEYWORDS CTORF261 gene; meca2 gene; meci gene; mecr1 gene; NTOF101; ORF142.
SOURCE Staphylococcus sciuri.
ORGANISM Staphylococcus sciuri
REFERENCE 1 (bases 1 to 6368)
AUTHORS Wu, S., de Lencastre, H. and Tomasz, A.
TITLE Genetic organization of the meca region in methicillin-susceptible
and methicillin-resistant strains of Staphylococcus sciuri
JOURNAL J. Bacteriol. 180 (2), 236-242 (1998)
MEDLINE 98101461
PUBMED 9440511
REFERENCE 2 (bases 1 to 6368)
AUTHORS Wu, S.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1997) S. Wu, Lab of Microbiology, The Rockefeller
University, 1230 York Avenue, New York NY 10021, USA
COMMENT Related sequences L14020, X52593, Y09223.
FEATURES
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BASE COUNT	2230	a	998	c	884	g	2256	t
ORIGIN								
Query Match	100.0%	Score 28:	DB 1:	Length 6368:				
Best Local Similarity	100.0%	Pctd. No. 0.6:						
Matches 28:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:				
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DB	4457	CAACTAACTATTGATGCTAAAGTTCAAA	4484					
RESULT 13								
SAMECAR11								
LOCUS	9047	bp	DNA	linear	BCT 16-JAN-1998			
DEFINITION	Staphylococcus aureus meca, mecI, mecI genes and ORF168, ORF142, ORF44, ORF145 and ORF224.							
ACCESSION	Y14051							
VERSION	Y14051.1	GI:2791983						
KEYWORDS	meca gene; mecI gene; mecI gene; ORF142; ORF145; ORF224; ORF44; PBP2a; repressor protein; transposase.							
SOURCE	Staphylococcus aureus							
ORGANISM	Bacteria; Firmicutes; Bacillales; Staphylococcus.							
REFERENCE	1 (bases 1 to 9047)							
AUTHORS	Wu, S.							
TITLE	Direct Submission							
JOURNAL	Submitted (27-JUN-1997) S. Wu, Laboratory of Microbiology, The Rockefeller University, 1230 York Avenue, New York, NY 10021, USA							
REFERENCE	2 (bases 1 to 9047)							
AUTHORS	Wu, S., de Lencastre, H. and Tomasz, A.							
TITLE	Genetic organization of the meca region in methicillin-susceptible and methicillin-resistant strains of Staphylococcus sciuri							
JOURNAL	J. Bacteriol. 180 (2), 236-242 (1998)							
MEDLINE	98101461							
PUBMED	9440511							
FEATURES								
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gene								

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CDS	complement(15524..5952) /note="ORF142" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="CAA74377.1" /db_xref="GI:2791988"	REFERENCE 1 Hiramatsu, K., Cui, L., Kuroda, M., and Ito, T. The emergence and evolution of methicillin-resistant Staphylococcus aureus Trends Microbiol. 9 (10), 486-493 (2001) 2 21482917
CDS	/db_xref="SPTRMBL:054520" /translation="MKYDDFLVGETFRTKSLHITTEELIQPATTFDPOYMHIDKEKAE OSRPGIJJASGMHTLSISPKLWBECKYGEHVAGTQMNVPKIPVYPCNTIYVIAE ITNKRKSIKENGVLTVSLSTYNEEELVFGGEVYALINNS" complement(16049..6183) /note="ORF44" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="CAA74378.1" /db_xref="GI:2791989"	JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNALS MEDLINE 21895198 3 (bases 1 to 21777) Xue, M. X., Ito, T., Hiramatsu, K., and Tienasastorn, C. Direct Submission Submitted (12-JUN-2001) Teruyo Ito, Juntendo University, Department of Bacteriology, Hongo 2-1-1, Bunkyo-ku, Tokyo 113-8421, Japan (E-mail:teruyobacmed.juntendo.ac.jp, Tel:81-3-5802-1041, Fax:81-3-5684-7830) location/Qualifiers 1..21777 /organism="Staphylococcus aureus" /strain="JCSG1978(8/6-3p)" /db_xref="taxon:1280" /note="community-acquired MRSA strain isolated at the University of Chicago children's hospital" 301..21221 /note="302..21222 or 303..21223 or 304..21224 type-IV SCCmec of JCSG1978(8/6-3p)" 301..326 /note="inverted complementary repeat(ir-I) of SCCmec of JCSG1978"
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REFERENCE Staphylococcus aureus
TITLE Bacteria: Firmicutes; Bacillales; Staphylococcus.
1 Hiramatsu, K., Cui, L., Kuroda, M. and Ito, T.
The emergence and evolution of methicillin-resistant Staphylococcus
aureus Microbiol. 9 (10), 486-493 (2001)
2 21482917
3 Ma, X., Ito, T., Tienasaitorn, C., Jamklang, M., Chongtrakool, P.,
Boyle-Vavra, S., Daum, R.S. and Hiramatsu, K.
Novel Type of Staphylococcal Cassette Chromosome mec Identified in
Community-Acquired Methicillin-Resistant Staphylococcus aureus
Strains Antimicrob. Agents Chemother. 46 (4), 1147-1152 (2002)
4 21895198
5 (bases 1 to 26090)
6 Xue, M., Ito, T., Hiramatsu, K. and Tienasaitorn, C.
Direct Submission
Submitted (12-JUN-2001) Teruyo Ito, Juntendo University, Department
of Bacteriology, Hongo 2-1-1, Bunkyo-ku, Tokyo 113-8421, Japan
(E-mail:teruybac@med.juntendo.ac.jp, Tel:81-3-5802-1041,
Fax:81-3-5684-7830)
On Mar 11, 2002 this sequence version replaced gi:17025971.
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